OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
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Run on: June 15, 2005, 02:16:48 ; Search time 183 Seconds
(without alignments)
10947.644 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 ctccgagattacccttacag.............ctccttccttcttcccctcc 2590

Scoring table: BLOSUM62
                    Xgapop 10.0 ; Xgapext 0.5
                    Ygapop 10.0 ; Ygapext 0.5
                    Fgapop   6.0 ; Fgapext 7.0
                    Delop   6.0 ; Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10775627/runat_14062005_140909_19272/app_query.fasta_1.2759
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-DB=A_Geneseq_16Dec04 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10775627 @CGN 1 1 194 @runat 14062005 140909 19272 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_16Dec04:*
              1: geneseqp1980s:*
              2: geneseqp1990s:*
              3: geneseqp2000s:*
              4: geneseqp2001s:*
              5: geneseqp2002s:*
              6: geneseqp2003as:*
              7: geneseqp2003bs:*
              8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2809	60.9	545	5	ABB08276	Abb08276 Murine mu
2	2359.5	51.2	548	6	ADB64489	Adb64489 Human pro
3	1922.5	41.7	452	6	AAE32210	Aae32210 Human cyt
4	1922.5	41.7	452	7	ADB64249	Adb64249 Human nov
5	1763	38.2	412	4	ADC31770	Adc31770 Human nov
6	1735.5	37.6	414	4	AAU15868	Aau15868 Human nov
7	1735.5	37.6	414	6	ABU54937	Abu54937 Human nov
8	1166	25.3	358	4	AAG63832	Aag63832 Amino aci
9	1166	25.3	358	4	AAG93278	Aag93278 Human pro
10	1166	25.3	358	7	ADC31154	Adc31154 Human nov

ALIGNMENTS

RESULT 1
ABB08276

ID   ABB08276 standard; protein; 545 AA.
XX
AC   ABB08276;
XX
DT   15-JUL-2002 (first entry)
XX
DE   Murine muscle ring finger protein 2 (MURF-2).
XX
KW   Muscle ring finger; MURF-2; mouse; cardiant; microtubule;
KW   intermediate filament; striated muscle; cardiac hypertrophy;
KW   heart disease.
XX
OS   Mus musculus.
XX
PN   WO200206318-A2.
XX
PD   24-JAN-2002.
XX
PF   18-JUL-2001; 2001WO-US022896.
XX
PR   18-JUL-2000; 2000US-0219020P.
XX
PA   (TEXA) UNIV TEXAS SYSTEM.
XX
PI   Olson EN, Spencer JA;
XX
DR   WPI; 2002-241506/29.
DR   N-PSDB; ABA99062.
XX
PT   Novel muscle ring finger protein useful for drug screening, and for
PT   diagnosing and treating diseases, particularly cardiomyopathies.

11	1162	25.2	366	5	ABB08275	Abb08275 Murine mu
12	1140.5	24.7	396	3	AAB21048	Aab21048 Human nuc
13	1139.5	24.7	366	4	AAU25438	Aau25438 Human mdd
14	1131	24.5	400	5	ABB81144	Abb81144 Human nov
15	1121	24.3	351	5	ABB81134	Abb81134 Rat MURF1
16	1095.5	23.8	370	4	AAM00918	Aam00918 Human bon
17	1088.5	23.6	353	4	ABB50234	Abb50234 Human tra
18	1088.5	23.6	353	6	ABG93804	Abg93804 Human bon
19	1088.5	23.6	353	6	ADA55293	Ada55293 Human pro
20	1088.5	23.6	353	7	ADE61549	Ade61549 Human nov
21	1088.5	23.6	353	7	ADE61546	Ade61546 Human Pro
22	1086	23.6	289	5	ABB81145	Abb81145 Human MUR
23	1086	23.6	340	5	ABB81135	Abb81135 Human MUR
24	1082.5	23.5	366	6	AAU15855	Aau15855 Human nov
25	1082.5	23.5	366	6	ABU54924	Abu54924 Human nov
26	1082	23.5	343	5	ABB08277	Abb08277 Murine mu
27	1022	22.2	302	5	ABB83475	Abb83475 Human cyt
28	949	20.6	254	4	AAM00998	Aam00998 Human bon
29	918	19.9	254	4	AAB61322	Aab61322 Human tra
30	871.5	18.9	602	8	ADP22642	Adp22642 Sea-squir
31	817	17.7	181	7	ADC33320	Adc33320 Human nov
32	788	17.1	201	5	ABB81142	Abb81142 Rat MURF1
33	786	17.0	184	6	AAU16327	Aau16327 Human nov
34	786	17.0	184	6	ABU55396	Abu55396 Human ORF
35	634.5	13.8	143	3	AAB41076	Aab41076 Human ORF
36	634.5	13.8	143	5	ABP34078	Abp34078 Human int
37	485	10.5	122	3	AAB41760	Aab41760 Human ORF
38	459	10.0	716	7	ADD01211	Add01211 Human nuc
39	448	9.7	719	6	ADA14349	Ada14349 Mouse spe
40	436	9.5	667	8	ADQ21458	Adq21458 Human sof
41	432.5	9.4	552	7	ADJ70562	Adj70562 Human hea
42	431	9.3	685	4	AAM79101	Aam79101 Human pro
43	431	9.3	685	6	ABG18060	Abg18060 Novel hum
44	431	9.3	744	4	ABG18061	Abg18061 Novel hum
45	420	9.1	524	8	ADR09855	Adr09855 Human pro

```
PS   Claim 42; Fig 10; 134pp; English.
XX
CC   The sequence represents murine muscle ring finger protein 2 (MURF-2). The
CC   invention relates to a purified muscle ring finger (MURF) protein,
CC   selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the
CC   invention are involved in microtubule and intermediate filament
CC   stabilisation of striated muscle cells and have cardiac activity. The
CC   MURF proteins are useful for screening a candidate substance for MURF
CC   protein-binding activity, in a cell, cell-free system or in vivo, and its
CC   effect on interaction of MURF with microtubules, homodimerisation of
CC   MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction
CC   of MURF with intermediate filaments, e.g. desmin, vimentin and
CC   cytokeratin, and heterodimerisation of MURF. The screened compounds are
CC   useful for treating and preventing cardiac hypertrophy and heart
CC   diseases. MURF proteins are useful as antigens to immunise animals for
CC   the production of antibodies
XX
SQ   Sequence 545 AA;
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Alignment Scores:

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Pred. No.:                       4.34e-227          Length:        545
Score:                 2809.00                      Matches:       545
Percent Similarity:     100.00%                     Conservative:    0
Best Local Similarity:  100.00%                     Mismatches:      0
Query Match:             60.92%                     Indels:          0
DB:                           5                     Gaps:            0
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US-10-775-627A-3 (1-2590) x ABB08276 (1-545)

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Qy    80  ATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGAGACGAGACCATGGATAACTTG  139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MetSerThrSerLeuAsnTyrLysSerPheSerLysGluGlnThrMetAspAsnLeu      20

Qy   140  GAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGCCTGTGGTCATTCTC   199
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Db    21  GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeu   40

Qy   200  CCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACATCTTCCAGGCCTTCTACCCG   259
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41  ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro   60

Qy   260  TACTTACCCACCAAAGAGAGGACCACCCGTGCCATCAGGGGCGCGCTTCCGTGTCCCTCC   319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TyrLeuProThrLysGluArgThrThrArgAlaIleArgGlyAlaLeuProCysProSer   80

Qy   320  TGCAGACATGAGGTGGTTGTTAGACACGAACATGGGGTCTATGGACTGCAGAGAACCTGCTC  379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81  CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu   100

Qy   380  GTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAGGCCACAGGCTCTATGGAC   439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101  ValGluAsnIleIleAspIleTyrLysGlnGluSerThrArgProGlyLeuTyrGlyAsp  120

Qy   440  CAGCCCCATGTGTGTGAAGAGCATGAAAGAATCAACATCTATTGTCTGAACTGTGAA   499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GlnProMetCysGluGluHisGluArgIleAsnIleTyrCysLeuAsnCysGlu       140

Qy   500  GTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAAGGACTGCCAGGTGGGCTCCC  559
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141  ValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGlnValGlyAlaPro 160

Qy   560  CTGACTCATGTGTTCCAGAGCGGAGAGTCAGTGAATTGCTGTACTTGTGTG          619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161  LeuThrHisValPheGlnArgGlnLysSerGlnSerArgAspProGlyIleLeuAlaValLeuVal 180

Qy   620  GGAAGCAACGATAGAGTCCAGGGTGTTGATCAGCGGACCACCTGTAAAACTATT      679
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GlySerAsnAspArgValGlnGlyValAspGlnArgThrThrCysLysThrIle       200

Qy   680  GAGGAGTGCTGCAGAAAGCAAAACAGGACCTGTGTGAGAAATTTGATCACCTATACGGC   739
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201  GluGluCysCysArgLysGlnAsnArgThrCysValArgAsnLeuIleThrTyrArgGly   220

Qy   740  ATCCTGGAGGAGGAAGACTGAAATGAACCCAAGCACCATCACTCACTCAGGAGGAGAA    799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221  IleLeuGluGluGluArgLysThrGluMetThrGlnAlaIleThrArgThrGlnGluGluLys 240

Qy   800  CTGGAACATGTCCAGAACTCTTATCGCAGGTAGATTCGGATCACCTGAGCAGAAGTATCCAAG 859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  LeuGluHisValArgThrLeuIleArgGlyArgLeuSerGlnLeuGluAsnValSerLys   260

Qy   860  TTGGTGGAGTCAGGAATCCAGTTCATCAGGATGAGGAGGCCGAAATGGCACGTATTTCTGCAGAAT 919
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261  LeuValGluSerGlyIleGlnLnPheMetAlaAspValProLeuGluAsn           280

Qy   920  GCCAAGACCCTGTTGCAAAAGATCGTGGAAGGCCATCAAAGGGCGTTTCAGATGGAAACTA  979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281  AlaLysThrLeuLeuGlnLysIleValGluAlaSerLysAlaPheGlnMetGluLysLeu   300

Qy   980  GAAACAAGGTTATGAGATCATTGAGATCTTCACTGTGCAATCTTCAATAGAGAGAAAAATT  1039
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GluGlnGlyTyrGluIleIleMetSerAsnPheThrValAsnLeuAsnArgGluGluLysIle 320

Qy  1040  ATCCGTGAAAATGACTTTTCTGAGGAGAGAAGAAGTCTGGAGGAGAAAGAGGAAAATGAT  1099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321  IleArgGluIleAspPheSerGluGluArgArgSerLeuGluGluLysGluGluAsn     340

Qy  1100  GAAGAAGGAGAAGAGGAGGATGCCAGTGAAGAAGAAGAGAGGGAGAAATGTTCAAAATAGCA 1159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341  GluGluGlyGluGluGluAspAlaSerGluGluGluArgArgGluLysCysSerLysIleAla 360

Qy  1160  TCTTCAGGGGAAGAGGAGGAGGTCTGGAGGAGGAGAAGTCTGGAGGAGAAGAGGAAAATAGAT 1219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  SerSerGlyGluGluGluValTrpArgArgArgSerGlyGlyGluGluLysSerGlyGluGlu 380

Qy  1220  CTTCAGGTGCGCCCCAGAGCCACTACCTGCTTCCTCTCCGAACCGTTTTCATCCATGCCA  1279
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Db   381  LeuGlnValAlaProProGluProAlaSerSerSerProGluProPheSerSerMetPro   400

Qy  1280  CCTGCTCGGATGTCTCTGGGTGACACACAGGGGGAGGGGGTGGTGCTCTTCGGCTCCAGAACC 1339
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401  ProAlaAlaAspValLeuValThrGlnGlyGluValValProIleGlySerGlnGluThr   420

Qy  1340  ACACAGTCTGAAAACTTCAGGCCTTCAGCACCGGGAAACTGCGGATCCCCTTGTTTTAACCCT 1399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ThrGlnSerGluThrSerGlyProSerAlaAlaGluThrArgAlaAspProLeuPheTyrPro 440

Qy  1400  AGTTGGTATAAAAGGCCCAAAGGCGAAAGCCCGGAAAAACCACACCTTGCCACTCCCATGGGAGT 1459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441  SerTrpTyrLysGlyGlnSerArgLysSerThrSerSerAsnProProCysThrHisGlySer 460

Qy  1460  GAAAGGTCTGGGGTCAAAATAGGGCCCTGGGCATTGAGAGCAGTCCAGTGTGCAGTCCGAGAA 1519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461  GluGlyLeuGlyLeuLysIleGlyProLeuGlyIleGluAspSerSerValGlnSerAlaGlu 480

Qy  1520  GTGGCACGAAAGCCGCAACCAATGAGCAGGCAGCTGGTGGTTAGTTCTGAGAGTCCTAGTTCAACT 1579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  ValAlaGlnLysAlaAlaThrAsnGluGlnAlaAlaValSerGlyLysSerSerSerThr   500

Qy  1580  GCAGGTACCTCCAGATTGGATTGGAGGCCCCTTCTCCCAGGGACAGCAGTCTTGCGCCTTG  1639
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Db   501  AlaAlaThrSerGlnIleGlyLeuGlyAlaProSerProGlnGlyGlnGlnSerAlaAlaLeu 520

Qy  1640  GGGAGTGGGGGTGGGGTTGATCCTGAGGCCAGTCGCGCCACGTTTTCTCCTGGTTTG     1699
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521  GlySerGlyGlyGlyValAspProGluAlaSerProAlaThrSerProGlyLeu       540

Qy  1700  AATTCCCTAAAATGAA  1714
          ||||||||||||||||
Db   541  AsnSerLeuAsnGlu    545
```

RESULT 2

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ID   ADB64489
XX
AC   ADB64489;
```

Db   541 AsnSerLeuAsnGlu   545

DB   ADB64489 standard; protein; 548 AA.

```
DT   04-DEC-2003  (first entry)
XX
DE   Human protein encoded by clone HEART20019310.
XX
KW   Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW   cell regeneration; membrane protein; signal transduction-related protein;
KW   transcription-related protein; osteoporosis; neurological disease;
KW   cancer; tumour.
XX
OS   Homo sapiens.
XX
PN   EP1308459-A2.
XX
PD   07-MAY-2003.
XX
PF   28-MAR-2002; 2002EP-00007401.
XX
PR   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-00350978.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI   Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI   Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
PT   New polynucleotides and polypeptides, useful for developing a diagnostic
PT   marker or medicines for regulation of their expression and activity, or
PT   as targets of gene therapy.
XX
PS   Claim 1; Page; 222pp; English.
XX
CC   The invention discloses a polynucleotide comprising a sequence selected
CC   from 1970 fully defined nucleotide sequences which encode novel
CC   polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC   or its partial peptide, immunologically assaying the polypeptide or peptide
CC   of the polynucleotide, an antibody binding to the polypeptide or peptide
CC   of the polynucleotide by contacting the polypeptide or peptide
CC   with the antibody of the encoded protein, and observing the binding
CC   between the two, a transformant carrying the polynucleotide in an
CC   expressible manner and an antisense polynucleotide. The oligonucleotide
CC   is useful as a primer for synthesising the polynucleotide, or as a probe
CC   for detecting the polynucleotide. The polynucleotides and encoded
CC   proteins are useful as pharmaceutical agents and many disease-related
CC   genes may be included in them, for developing a diagnostic marker or
CC   medicines for regulation of their expression and activity, or as targets
CC   of gene therapy. The genes are involved in tissue and/or cell
CC   regeneration. Membrane proteins, signal transduction-related proteins,
CC   transcription-related proteins, disease-related proteins and genes
CC   encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC   neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC   the activity or expression of the encoded protein to treat diseases. The
CC   sequence presented is a protein of the invention. Note: Some of the
CC   sequence data for this patent is not represented in the printed
CC   specification, but is based on sequence information supplied by the
CC   European Patent Office.
XX
SQ   Sequence 548 AA;

Alignment Scores:
Pred. No.:       3.02e-189
Score:           2359.50          Length:       548
Percent Similarity: 90.56%        Matches:      465
Best Local Similarity: 84.39%     Conservative: 34
Query Match:     51.17%           Mismatches:   44
                                  Indels:       9
DB:  WPI; 2003-450961/43.         Gaps:         3
     N-PSDB; ADB62519.
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US-10-775-627A-3 (1-2590) x ADB64489 (1-548)

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Qy          1 ATGAGCGCACTTCTCTGAAATTACAAGTCTTTTCTCCAAAGAGCCAGCAGACCATGGATAACTTG 139
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetSerAlaSerLeuLeuAsnTyrLysSerPheSerArgLysGlnGlnThrMetAspAsnLeu 20

Qy         80 GAAAAGCAACTGACTTGTCCCATCTGCCTCAGAGATGTTCAGGAGGCTTCACGAAGCCTGTCATTCTC 199
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db         21 GluLysGlnLeuLeuCysProIleCysLeuGluMetPheThrLysProValValLeuLeu 40

Qy        140 TACTTACCCACACAGAGGAGGGAGGGCACCACCACCGTGGGCCATCAGGGGGCGCCTTCCGGTGTCCCTCC 199
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerArgLysArgAspAlaSerArgAsnPro 60

Qy        200 CCTTGCCAGCACAACCTGTGCCGTAAAAGATGTGCCAGTAAGAGAGATGCTTCTCGGAATCCG 259
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TyrLeuProThrArgGlyGlyThrThrMetAlaSerGlyGlyAlaProPheArgCysProSer 80

Qy        260 CAGCCCAGTGTGAAGAGCATGAAGAAGCATCAACACTCTATTGTCTCGAACTGTGAA 319
              |||||||||||||||||||||||||||||||||||||||||||||::|||||||||||
Db         81 CysArgHisGlnAlaValLeuAspArgHisGlyGlyTyrArgGlyLeuGlnArgAsnLeuLeu 100

Qy        320 TGCAGGACATGAGGTGGTTGTTAGACACAGACATGGGTGTCTATGGACTGCAGAAACTGCTC 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ValGluAsnIleIleAspLeuTyrLysGlnLeuSerThrArgProGlyLysLysSerAsp 120

Qy        380 GTGGCCACCTCTTCCTTGTGCAAGGGTTTTTCGGCGCCCCATAAGGACTGCCCAGTGGCTCC 439
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GlnProMetCysGluGluLeuGluGluLeuGlnArgIleAsnIleTyrCysLeuAsnCysGlu 140

Qy        440 CTGACTCATCTGTTCCAGGAGGCAGAAGTCAGGAGCTCAGTGAGTGGTATTGCTACTTGTG 499
              |||||||||||||||||||||||||||||||||||||||||||||||||||||::|||||||
Db        141 ValProThrCysSerLeuCysLysLysValPheGlyAlaHisLysAspCysGlnValAlaPro 160

Qy        500 GTGGGAAAACAATTATTGATACTTACAAGCACGAGAATCCACAGGCCCAGAAAAAAATTGGAC 439
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Db        161 LeuThrHisValPheGlnIleLysGlnGlnLeuSerGluAspGlyIleAlaIleLeuVal 180

Qy        560 CTGGAAGGCAACGATAGAGTCCAGGGTGTGATCAGCCACTGTGGAGGACACCTGTAAAACTTATT 619
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db        181 GlySerAsnAspArgValGlnGlyValIleSerHisCysGlyGlyHisLeuThrIle 200

Qy        620 GGAGGAGTGCTGCAGAAAGCAGAAACAGGACCTGTGTGAGAAATTTGATCACCTATACGGC 679
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GluGluCysSerArgLysGlyGlnLysGlnLeuCysGluLysPheAspThrLeuTyrGly 220

Qy        680 ATCCTGGAGGAGGAAGAGACTGAAATGACCCAAGCCATCATCACTCGAACACAGGAGGAGAAA 739
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 IleLeuGluGluGluGluThrGluMetThrGlnAlaIleIleThrArgThrGlnGluGluLys 240

Qy        740 CTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCACACCTGGGAGCAAGGTATCCAAG 799
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LeuGluHisValArgThrLeuIleArgLysTyrSerAspHisThrTrpGluGlnValSerLys 260

Qy        800 TTGGTGGAGTCAGGAATCCACTTCATGGAATGAGCCCGAAATGGCAGTATTCTGCAGAAT 859
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        261 LeuValGluSerGlyIleGlnPheMetAspGluProGluMetAlaValPheLeuGlnAsn 280

Qy        860 GCCAAGAGCCCTGTTCGTTGCAAAAGATCTGGAAGCCATCAAAGCCGTTTCAGATGGAGAACTA 919
              |||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        281 AlaLysSerProLeuLeuGlyLeuIleSerGluAlaSerLysAlaPheGlnMetGluAsnIle 300

Qy        920 GAACAAGGTTATGAGATCAATGAGCAACTTCACTGTCAAATCTCAATAGAGAAGAGAAAAATT 979
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        301 GluHisGlyTyrGluIleAsnMetAsnHisLeuHisCysGlnIleSerIleGluLysArgLysIle 320

Qy        980 ATCCGTGAAATTGACTTTCTGA------GAAGAGGAAGAGGAAGAGGATGCCAGGAA 1039
              ||:||||||||||||||||||||      |||::|||||||||||||||||||||||||
Db        321 IleArgGluIleAspPheTyrArgGluAspGluAspGluGluGluGluAspGlyGlyGluGly 340

Qy       1040 ATAGAGTGAAGGAAGAGGAGGAAGAGGAGGAGGAG----------GATGCAGTAGAGTAGGAAGAGGAAGAGGAGGAG 1094
              ::||||||||||||||||||||||||||||||||||          |||:|||||:||||||||||||||||||||
Db        341 GlyGluGlyGluGluGlyValGlyGlyGluValGlyGlyGluValGlyGluValGlu 360
```

```
Qy   1145  AATGTTCAAATAGACATCTTCAGGGGAGAAGAGAGTCTGGGAGAGAAAGCTGCAGAGCCCTCT  1204
                 |||:::  ||||||||||||    ||||||:::||:::||
Db    361  AsnValGlnThrGluPheProGlyGluAspGluAsnProGlyGluLysAlaSerGluLeuSer  380

Qy   1205  CAGCCTTCCCGCAGAGCTTCAGTCGCCCAGAGCCACTACCTGCTTCCTTCCTCCAGAACCG  1264
                 |||:::    |||||||||||||||||||||||||||
Db    381  GlnVal----------GluLeuGlnAlaAlaProGlyAlaLeuProValSerSerProGluPro  398

Qy   1265  TTTTCATCCATGCCACCTGCTTGCAGATGTCCTGGTGTGACACAGGGGGAGGTGGTGCCCATT  1324
                 :|:::|||||||||||||
Db    399  ProProAlaLeuProProAlaAlaAlaProValThrGlnGlyGluValValProThr  418

Qy   1325  GGCTCTCAGCAGAACCACACAGTCTGAAACTTCAGGCCCCTCAGCACGGAAACTGCGGAT  1384
                 |||||:::|||||||||||||
Db    419  GlySerGluGlnThrThrGlnLeuGlyIleGlyProProGlySerGluAspSerAsn  438

Qy   1385  CCCTTGTTTTACCCTAGTTGGTATAAAAGGCCAAAGCCGGAAAACACAGCTCCAACCCACCT  1444
                 |||||:::|||||||||||||
Db    439  ProLeuPheTyrProSerTrpTyrLysGlyGlnThrThrArgAsnProPro  458

Qy   1445  TGCACTCATGGGAGTGGGAGTGTCTGGGTCAAATAGGGCCCTCTGGGCATTGAGGATTCCAGT  1504
                 |||||:::|||||||:::|
Db    459  CysThrProGlySerGluGlyLeuGlyIleLeuGlyValGluAspSerAsn  478

Qy   1505  GTGCAGTCCGCAGAAGTGGCAGAAGCCGCAACCAATGAGCAGCCAGTGAGTGGTAAG  1564
                 |||||:::||||||||||||||||||||||
Db    479  ValArgLysAlaGluValAlaAlaAlaSerGlnValArgLysCysSerProLeuLys  498

Qy   1565  GAGTCTAGTTCAACTGCAGCTACCTCTCAGATTGGATTGGAGGCCCTTCTCCCCAGGGA  1624
                 :::|||:::||||||:::|
Db    499  GluThrSerSerAlaProAlaAlaThrSerGlnIleGlyPheGluAlaProProLeuGlnGly  518

Qy   1625  CAGTCTTGCAGCCTTGCGGAGTGGGGGTGGGGT-GATCCTGAGCCAGCTCCGCCAGCTGTCTTC  1683
                 ||||||||:::|||||||||||||||||
Db    519  GlnAlaAlaLeuAlaProAlaSerGlyLysGlyAlaAspSerGlyLeuProAlaAlaArgHisIlePhe  538

Qy   1684  TCCTTCTCCTTGGTTTGAATTCCCTAAATGAA  1714
                 |||||||||||||||||||||
Db    539  SerPheSerTrpLeuAsnSerLeuAsnGlu  548
```

```
Alignment Scores:
Pred. No.:                                 1.7e-152    Length:          452
Score:                                     1922.50     Matches:         392
Percent Similarity:                        75.14%      Conservative:     22
Best Local Similarity:                     71.14%      Mismatches:       33
Query Match:                               41.69%      Indels:          105
DB:                                        6           Gaps:              4

US-10-775-627A-3 (1-2590) x AAB32110 (1-452)

Qy      1  ATGAGACACTTCTCTGAATTACAAAGTCTTTTCTCCCAAAGAGAGCAGCAGACCATGGATAACCG   139
           |||||||
Db      1  MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnThrMetAspAsnLeu   20

Qy     80  CCCTTGCCAGCACCAACCTGTTGCAGGAGAAATGTCCAGTGACATCTTCCAGGCCCTCTAACCG   139
           |||||
Db     41  ProCysGlnHisAsnLeuCysArgLysCysSerAlaSerArgAspIlePheGluGlnAlaSerAsnPro   60

Qy    140  GAAAAAGCAACTCAATCGTCTCCCATCTCCGCTAGAAGATGTTCACGAAGCCTGTGGTCATTCTC   199
           |||||
Db     21  GluLysGlnLeuLeuCysSerProIleCysLeuGluMetPheThrLysProValValIleLeu   40

Qy    140  GAAAAAGCAACTCAATCGTCTCCCATCTCCGCTAGAAGATGTTCACGAAGCCTGTGGTCATTCTC   199
           |||||
Db     21  GluLysGlnLeuLeuCysSerProIleCysLeuGluMetPheThrLysProValValIleLeu   40

Qy    200  TACTTACCCACAAAGAGGAGGACCACCGTGGGAGTCCCCAGCGATCAGGGGGCCGCTTCCGG   319
           |||||
Db     61  TyrLeuProThrArgGlyGlyThrThrMetAlaSerGlyIleGlyArgPheArgCysProSer   80

Qy    320  TGCAGACATGAGGTGGTGGTTGTTAGACAGACCATGGGGTCCATATGACTGCGAGGAACCTCTC   379
           |||||
Db     81  CysArgHisGluValValLeuAspArgHisGlyValThrTyrGlyValLeuArgAsnLeuLeu   100

Qy    380  GTGGAGAAACATTATTGTGATATCTGTACAAGCAGAAATCCACCAGGCCCAGAAAAAATTGGAC   439
           |||||
Db    101  ValGluAsnIleIleAspIleTyrLysGlnValThrArgProGlyIleAlaIleLeuVal   120

Qy    440  CAGCCCATGTGTGAAAGCACATGAAGAGAAGCCATCAACATCTATTGTCTGAACTGTGAA   499
           |||||
Db    121  GlnProMetCysGluSerGluHisGluGluLysProSerThrSerIleValEnd   140

Qy    500  GTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGACATAACGGACTGCAGCTGGGGCTCC   559
           |||||
Db    141  ValProThrCysSerLeuCysLysValPheGlyAspIleThrAspCysSerTrpGlySer   160

Qy    560  CTGACTCATGTGTTCCAGAGACAGAAGTCAGAGCTCAGTGATGGTATTGTTGTTACTTGTG   619
           |||||
Db    161  LeuThrHisValPheGlnArgGlnLysSerGluLeuSerAspGlyIleValValThrCys   180

Qy    620  GGAAGCAAGCGATTAGAGTCCAGGGTGTTGATCAGCCAGTGGAGGAACACCTGTAAAACTATT   679
           |||||
Db    181  GlySerAsnAspArgValGlnGlyValIleSerGlnValAspThrCysLysThrIle   200
```

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: June 15, 2005, 04:49:37 ; Search time 58 Seconds
(without alignments)
8593.152 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 ctcgagattacccttacag.........ctccttccttcttcctcc 2590

Scoring table: BLOSUM62
 Xgapop 10.0 ; Xgapext 0.5
 Ygapop 10.0 ; Ygapext 0.5
 Fgapop 6.0 ; Fgapext 7.0
 Delop 6.0 ; Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10775627/runat_14062005_140910_19292/app_query.fasta_1.2759
-DB=PIR_79 -QFMT=faatan -SUFFIX=rpt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-OUTFMT=pto -NORM=ext -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN-20 -MODE=LOCAL
-USER=US10775627@CGN_1_1_66 @runat_14062005_140910_19292 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	442	9.6	667	2	T09013	RING finger protei
2	436	9.5	667	2	T09482	ring finger protei
3	259	5.5	624	2	S28418	probable zinc-bind
4	253	5.5	551	2	JC7562	glioblastoma RING
5	253	5.5	609	2	A43906	nuclear phosphopro
6	246.5	5.3	792	2	T00082	hypothetical prote
7	224	4.9	518	2	JC7387	testis-abundant fi
8	223.5	4.8	574	2	S28275	hypothetical prote
9	223.5	4.8	974	2	E88549	protein F54G8.4 [i
10	220.5	4.8	365	2	A30891	regulatory protein
11	212	4.6	477	2	JE0343	terf protein - rat
12	211.5	4.6	506	2	S37583	RING finger protei
13	208	4.5	801	4	TVHURE	transforming prote
14	207.5	4.5	513	1	TVHURF	ret finger protein
15	206	4.5	475	1	A37241	52K autoantigen Ro
16	205.5	4.5	442	2	A57041	transcription regu
17	204	4.4	630	2	A49656	estrogen-responsiv
18	200.5	4.3	1234	2	T00363	hypothetical prote
19	200	4.3	634	2	I49642	estrogen-responsiv
20	189	4.1	375	2	F88947	protein C39F7.2 [i
21	189	4.1	375	2	T33778	hypothetical prote
22	187.5	4.1	892	2	T09071	hypothetical prote
23	187	4.1	676	2	JC7222	77K muscle-derived
24	186.5	4.0	698	2	T32840	SH3 domains-contai
25	179.5	3.9	2346	2	T13829	hypothetical prote
26	177	3.8	1051	2	S55259	Tpr homolog - mou
27	174.5	3.8	662	2	T8233	TIF1 protein - mou
28	172.5	3.7	574	2	A46054	probable transcrip
29	171.5	3.7	412	2	D88072	GTP-binding protei
30	171.5	3.7	955	4	C40045	protein ZK1240.1 [
31	169.5	3.7	775	2	D86261	probable transcrip
32	169	3.7	1110	2	I51116	hypothetical prote
33	165	3.6	1020	1	QFHUH	NF-180 - sea lampr
34	164	3.6	802	2	S42518	neurofilament trip
35	164	3.6	802	2	S44382	PML protein, splic
36	162.5	3.6	3507	2	T34513	PML protein, splic
37	161	3.5	1322	2	T15689	hypothetical prote
38	159.5	3.5	2924	2	T18378	variant-specific s
39	158.5	3.4	633	2	S19244	gene Myl protein -
40	158.5	3.4	860	2	S44380	PML protein, splic
41	158.5	3.4	860	2	S42516	PML protein, splic
42	158.5	3.4	906	2	T00039	hypothetical prote
43	157.5	3.4	292	2	T32000	hypothetical prote
44	157.5	3.4	589	2	S42517	PML protein, splic
45	157.5	3.4	641	2	A40045	probable transcrip

ALIGNMENTS

RESULT 1
T09013
RING finger protein Fxy - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C;Accession: T09013
R;Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A;Title: A gene spans the pseudoautosomal boundary in mice.
A;Reference number: Z16531; MUID:98004518; PMID:9342357
A;Accession: T09013
A;Gene: Fxy
A;Molecule type: mRNA
A;Residues: 1-667 <PAL>
C;Cross-references: EMBL:AF026565; NID:g2589222; PIDN:AAB83986.1; PID:g2589223
C;Genetics:
A;Gene: Fxy
A;Map position: X; Y
C;Superfamily: rfp transforming protein
C;Keywords: zinc finger
F;6-65/Domain: RING finger homology <RRN>

US-10-775-627A-3 (1-2590) x T09013 (1-667)

Alignment Scores:
Pred. No.: 2.61e-21
Score: 442.00
Percent Similarity: 39.74%
Best Local Similarity: 23.72%
Query Match: 9.59%
DB: 2

Length: 667
Matches: 148
Conservative: 100
Mismatches: 188
Indels: 188
Gaps: 19

Qy 128 ATGGATAAACTTGGGAAAAGCAACTAACTGATCTGTTCCCATCTGCCTTAGAGATGTTCACGAAGCCT 187
    |||:|:|| ||||| |||| ::|| |||||| |||| :|||||:||:|| ||
Db 1 MetGluThrLeuGluSerGluLeuThrCysProIleCysLeuGluLeuPheGluAspPro 20

Qy 188 GTGGTCATTCTCCCTTGCCAGCACACAACCTGTGCAGGAAAATGTGCCAGTGACATCTTCCAG 247
    ::|||| |||||| |||| ::|||| ||||| |||
Db 188

```
Db    21  ---LeuLeuLeuProCysAlaHisSerLeuGlnPheAsnCysAlaHisArgIleLeuVal        39
Qy   248  ----GCCTCTAACCCGTACTTACCCACAGAGAGGAGGCCACCACCGTGGCATCGGG          298
Db    40  SerHisCysAlaThrAsn----------GluProValGluSerIle                    51
Qy   299  GGCCGGCTTCCGCGTTCCGCTCCTGCAGACATGAGGTGGTGTTAGACACATGGGGGTCTAT    358
Db    52  AsnAlaPheGlnCysSerProThrCysArgHisValIleThrLeuSerGlnArgGlyLeuAsp   71
Qy   359  GGACTCCAGAGGAACCTGGTGGGAAAACATTATTGATATATTACACAGGAATCC---        415
Db    72  GlyLeuLysArgAsnValThrLeuGlnAsnIleIleAspArgPheGlnLysAlaSerVal      91
Qy   415  -----                                                            415
Db    92  SerGlyProAsnSerProSerGluThrArgGlyArgAlaPheAspAlaAsnThrMet        111
Qy   415  -----                                                            415
Db   112  SerSerAlaGlyLysValLeuCysValLeuAspPheAlaValAla                   131
Qy   416  ------                                                           416
Db   132  LysThrCysValThrCysGlyValSerTyrCysGlyCysLeuLysAlaThrHisPro       151
Qy   449  ------                                                           449
Db   152  AsnLysLysProPheThrGlyHisArgLeuIleGluProLeuProAspSerHisIleLeuArg  171
Qy   172  GlyLeuThrCysLeuGluHisGluAspGluLysValAsnMetTyrCysValThrAspAsp     191
Db   500  GTGCCCACCCGTTCCTTGTGCAAGGTTTTTGGCGCCCATAAGGACTGCTGCCAGGTGGCTCCC  559
Qy   192  GlnLeuIleLeuCysAlaLeuCysGlyLysLysGlyIleAlaArgHisSerGlnHisValAlaAla 211
Db   425  GAAAAAAAA----TTGGACCAGGCCATG                                     448
Qy   425  ------                                                           415
Db   560  CTGACTCATGTGTTCCGAGAGGCCATGAAGAAGAAGGCCATCAACATCTATTGTGTTACTGTG  619
Qy   212  LeuSerGluArgTyrAspLysLysLeuGlnAsnLeuGluSerAsnLeuThrAsnLeuIle     231
Db   232  LysArgAsnThrGluLeuGlnThrLeuArgLeuLeuAlaLysLeuGlnInThrCysGlnHisVal 251
Qy   680  GGAAGCAACGATAGAGTCCAGGGTGTGATCAGCCACGGTGGAGCCACCGTAAAACTATT     679
Db   252  GluValAsnAlaSerArgGlnGluValAlaLysSerLeuThrGlnLysLeuIleGluGlu     271
Qy   740  ATCCTGGAGGAGGAGGAGGAGGACTGAGAAATGACCCAAGCCATC----ACTCGAACACAGAGGAG 796
Db   272  IleLeuGluGlnIleAsnArg----------GlnIleGluGlyTyrThrLysLysIleGlyGly 287
Qy   797  AAACTGGAACAGTCCGGAACTCTTATCAGGAAGTAATTCCGAT----CACTTGGAG          847
Db   288  LysValIleLeuArgLeuArgGlyLeuLeuAlaGlnInIleIleAlaAsnCysAlaLysGlnCysLeuGlu 307
Qy   848  AACGTATCCAAGTTGTGTGGAGTCAGGAATCCAGTTCATGGAATGCCCGAAATGGCAGTA    907
Db   308  ArgSerAlaSerLeuIleSerGlnAlaGluHisSerSerLeuUlyAsnAspHisAlaArg     327
Qy   908  TTTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAAGCGTTTCAG    967
Db   328  PheLeuGlnThrAlaLysAsnIleThrGluAlaValSerMetAlaThrAlaLeuSerSerGln  347
Qy   968  ATGGAGAACTAGAACAAAAGGTTAT---GAGATCAATAGCAAGCAACTTCACTGTCAATCTCAAT 1024
Db   348  ValLeuIleProGluIleLeuAsnAsnAspThrPheAlaLeuAspPheSer              367
Qy  1025  AGAGAGGAAAAAATTATTCCGTGAAAATTGACTTT-----                         1060
Db   368  ArgGluLysLysLeuGluLysGluLeuAspTyrLeuThrAlaProAsnProProAlaIle     387
Qy  1061  AGAGAGGAGGAGGAAGAGGAAGAAGAGATGCAGAGGAAAATAGATGAAGAAGAGGAGGAGGAT 1120
Db   388  ArgGluGlyLeuCysThrAlaSerTyrAspThrIleThrValHisTrpThrSerGluAsp     407
Qy  1121  GCAGTAGGAAGTA----------                                          1147
Db   408  GluPheSerValValSerTyrGluLeuGlnTyrThrIleGlnAlaAsnVal              427
Qy  1148  GTTCAAAATAGCATCTTCAGGGGTGGGGAAGAG----------                      1174
Db   428  ValSerLeuCysAsnSerAlaAspSerTrpMetIleValProAsnIleLysGlnAsnHis     447
Qy  1175  ----------                                                       1175
Db   448  TyrThrValHisGlyLeuGlnSerGlyTyrThrIleLysTyrIlePhePheThrValLysAlaIleAsn 467
Qy  1175  -----  GAGAGGTGGAG                                               1186
Db   468  GlnAsnGlySerArgSerGluProGlyLysLeuThrAsnSerGlnProProPheArg        487
Qy  1187  AAAGCTGCAGAGCCCTTCCCGCAGCTTCCCGAGGTCGCCCCCAGAGCCACTA---         1243
Db   488  LeuAspProLysSerGlyProAlaHisIleArgLysLysIleGlyValSerIleSerProAsnLeuThrValGlu 507
Qy  1244  -----  CCTGCTTCC                                                  1252
Db   508  ArgAspGluSerSerLysGlySerHisSerAlaProLysGluArgPheAlaGlyLySerSer   527
Qy  1253  ----------  TCTCCAGAACCGTTTTCA----------                          1273
Db   528  TyrGlyValAlaGlyAsnValPheIleLeuAspSerArgGlyArgHisSerTyrTrpProValValThr 547
Qy  1274  ATGCCACCTGCTCGCAGATGTCCCGGTGGTGACACAGGGG----------              1321
Db   548  SerGlyArgGlySerThrTrpTyrAlaIleGlyLeuAlaThrTyrArgSerAlaProLysHisGluTrp 567
Qy  1322  ATTGGCTCT----------  CAGCAGCACCACAGTCGTGAAACT                      1354
Db   568  IleLeuGlyLysAsnAlaAlaSerTrpAlaLeuCysArgCysHisSerAsnHisSerTrpAlaValValArg 587
Qy  1355  TCAGGGCCTTCAGCACGGGAAACTGGGGAYCTCCGGATCCCTGTTTTTACCCTAGTTGGTATAAGGC 1414
Db   588  HisAspGlyLysGluThrProIleLeuAlaProAlaProAlaProHis----LeuArgArg     603
Qy  1415  CAAAAGCCGGAAAACCAGCTCCAACCACCACCTTGCACTCACTGGGAGTGAAAGGTCGGGGTCAA 1474
Db   604  ValGlyValLeu                                                     607
Qy  1475  ATAGGGCCTCTG                                                     1486
```

RESULT 2

T09482

ring finger protein FXY - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09482

R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.

submitted to the EMBL Data Library, November 1997

A;Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of the

A;Reference number: Z16687

A;Accession: T09482

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-667 <PER>

A;Cross-references: UNIPROT:O15344; EMBL:AF035360; NID:g2827993; PID:g2827994

A;Map position: Xp22.3

C;Genetics:

A;Gene: FXY

C;Superfamily: rfp transforming protein

F;6-65/Domain: RING finger homology <RRN>

Alignment Scores:

Pred. No.:   6.5e-21   Length: 667

Score: 436.00   Matches: 146

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Percent Similarity:    39.90%        Conservative:  103
Best Local Similarity: 23.40%        Mismatches:    187
Query Match:            9.46%        Indels:        188
DB:                     2            Gaps:           19

US-10-775-627A-3 (1-2590) x T09482 (1-667)

Qy  128 ATGGATAACTTGGAAAAGCAAACTGAACTCTGTCCCATCTGCCTAGAGTGTTCACGAAGCCT 187
            |||:::  |||  |: ::  |||   ::|   :||  :::      ::||||||
Db    1 ------MetGluThrLeuGluSerGluLeuThrCysProIleCysLeuGluLeuPheGluAspPro 20

Qy  188 GTGGTCATTCCCTTGCCAGCACAACCTGTGCAGACAAAGTGCCAGTGACATCTTCCAG 247
            |||  ||| |:::  |:   ::|   |:|| : ||||||||||||||||||
Db   21 ---LeuLeuLeuProCysAlaHisSerLeuCysPheAsnCysAlaHisArgIleLeuVal 39

Qy  248 ---GCCCTTAACCCGTACTTACCCACCACAAGAGGCACCACCCTGGGCAATCAGGG 298
           ||| ::|  :||| |||  ::|   :|::
Db   40 SerHisCysAlaThrAsn------------------------GluSerValGluSerIle 51

Qy  299 GGCCGGCTTCCGGCTGCTCCCTGGTGGTGTTGAACAGACAGACATGGGGTCTAT 358
           ||||  ||::|||  :|||  : ::   :|   |::  :||  ||||  :|:
Db   52 ThrAlaPheGlnCysProThrCysArgHisValIleLeuThrLeuSerGlnArgGlyValLeuAsp 71

Qy  359 GGACTGCAGAGGACCTGCTCGTGGAAAACATTATTGATATNTCACAAGCAGGAATCC--- 415
           ||||||||||||||||||| |:||||| :||::::|| | :::|||  |||::|
Db   72 GlyLeuLysArgAsnValThrLeuGlnAsnIleIleGluAspArgPheGlnLysAlaSerVal 91

Qy  415 ---------------------------------------------------------- 415
Db   92 SerGlyProAsnSerProSerGluThrArgArgGluArgAlaPheAspAlaAsnThrMet 111

Qy  112 ThrSerAlaGluLysValLeuCysGlnPheCysAspProAlaGlnAspProAlaVal 131
Db  415 --------------------------------------------------------- 415

Qy  416 ---------------------------ACCAGGCCA 424
                                      ||
Db  132 LysThrCysValThrCysGluValValSerTyrCysSerAspGluCysLeuLeuAlaThrHisPro 151

Qy  425 GAAAAAAAAA-------------TTGGACCAGGCCC- 445
        |||||||||              :::|| ||||
Db  152 AsnLysAspProPheThrGlyHisArgLeuIleGluProCysAspSerHisArg 171

Qy  446 -------ATGTGTGAAGAGAGCAGCATGAAGAAGAAGCGCAATCTTATTGTCGAACTGTGA 499
               ||:|| |||||  |||  :||:||   :|:::    |:|| ::|||
Db  172 GlyLeuMetCysLeuGluHisGluAspGluLysGlyLysArgHisArgIleValAlaAla 191

Qy  500 GTGCCACCTGTTCCTTGTCCAAGGTTTTTGGGCGCCCATAAGGACTGCCAGGTGGCTCCC 559
           |||||   |||||  ::|:|| :|:||:||  ::| |||  |||  ::||||::
Db  192 GlnLeuIleLeuCysAlaLeuGluLysGlyArgHisArgHisGlnValAlaAla 211

Qy  560 CTGACTCANTGTTGTTCAGAGGCAGAGTCTCAGTGATGTTATTGCTGTACTGTG 619
           |||  ||   :||:|  |||| :::||  |:|: ||: ||||:|
Db  212 LeuSerGluArgTyrAspSerLeuArgHisAsnLeuGluSerAsnLeuThrAsnLeuIle 231

Qy  620 GGAGCAACGGATAGAGTCCAGGGTGTGATCAGGACCTGTAAAACTATT 679
           ||| ||  |::   :||||:||  ||||:  :|| |::|:::
Db  232 LysArgAsnThrGluLeuGluThrLeuLeuLeuLysLeuGlnThrCysGlnHisVal 251

Qy  680 GAGGAGTGCTGCAGAAAGCAGAAACAGAGGACTTGCTGTGAGAAATTTGATCACCTATACGGC 739
           |||||||||   ::| |: |||  |:|  |:||:||:|| :|:||::||  ||::|:
Db  252 GluValAsnAlaSerArgGlnValAlaLysSerLeuThrCysAspLeuLeuGlu 271

Qy  740 ATCCTGGAGGAGGAGGAAGCTGAAATGACCCAAGCCATC---ACTGCACACAGGAGGAG 796
           |:|||||||||||||||  |:|| |:|  :||  ||| :   ||: :||| |||||||
Db  272 IleLeuLeuGlnLnArg------------GlnIleIleGlyTyrThrLysIleLysGly 287

Qy  797 AAACTGGAACATGTCGGAACTCTTATCAGGAAGTATTCCGAT---------CACCTGGAG 847
           |||||||| ||| || ||||   :|:| ::||||:::     |||||||
Db  288 LysValMetArgLeuArgLysLeuAlaGlnGlnIleAlaAsnCysLysGlnCysIleGlu 307

Qy  848 AACGTATTCCAAGTTGGTGTGGAGTCAGGAAATCCAGTTCATTGGATGATGACCCGAAATGGCAGTA 907
           :::   ||:|| ||| :||:|||| |||||||||| ||::|||  ::|:|||  :||||:||:|
Db  308 ArgSerAlaSerLeuIleSerGlnHisAlaGluHisSerLeuLysGluAsnAspHisAlaArg 327

Qy  908 TTTCTGCAGAATGCCAAGACCCTTGCAAAAGATACGTGGAAGACATCGAAGCCGTTTCAG 967
           |||  |||| ||| |||::|  :::|| :|:|||   ::|||| ||  ||:||||: :||
Db  328 PheLeuGlnThrAlaLysAsnIleThrGluArgValSerMetAlaThrAlaSerSerGln 347

Qy  968 ATGGAGAAACTAGAACAAGGTTAT---GAGATCANTGAGAGCAAACTTCACTGTCAATTCAAT 1024
        ::: :|| |||||||||:||:||    ::||: |::|:|:||| ::|  :||: |:|
Db  348 ValLeuIleProGluIleAsnLeuAsnAspThrPheAlaLeuLeuAspAspSer 367

Qy 1025 AGAAGGAAGAAAAAAATTATCCGTGAAATTGACTTT----TCT 1060
        |:||||||| |:::::|||  ::||||:||:||      |||
Db  368 ArgGluLysLysLeuGluLeuGluLeuCysLeuAspThrTyrLeuLeuThrAlaProAsnProThrIle 387

Qy 1061 AGAGAAGGAAGAAGAAGAGAGAGAGAGAATAGATGAAGAAGAAAATAGAGATGGAGAAGAAGAAGGAGAT 1120
        |||||||||||||||||||||||||| |||  :|||||||| ||  :||:||||||||||
Db  388 ArgGluGluLeuCysThrArgAlaSerTyrArgAspThrIleThrValHisThrSerAspAsp 407

Qy 1121 GCAGTAGAGTA------------------------GAAGAGCAGAAAAT 1147
        ||||:|||:|                         :||:|||||||||
Db  408 GluPheSerValValSerTyrGluLeuGlnTyrThrIlePhePheThrGlyIleAlaAsnVal 427

Qy 1148 GTTCAAATAGCATCTCTTCCAGGGGAAGAG------------------------- 1174
        |||  :|| |||:|| :|||  ::|||:||
Db  428 ValSerLeuCysAsnSerAlaAspSerTrpMetIleValProAsnIleLysGlnAsnHis 447

Qy 1175 ---------------------------------GAGAGTCTGGAG 1186
                                         ||||||:||:||
Db  448 LeuAspProLysSerAlaHisArgLysValSerHisArgAspAsnLeuThrValGlu 467

Qy 1187 AAACTGCAGAGCCCTCTCCAGCTTCCCCGAGAGCTTCAGGTGCGCCCCAAGCCACT 1243
        ||:||||||||:|||||||||:||:||||||| :|||||||:| ::||||::||:|
Db  468 GlnAlaGlySerArgGluProGlyLysLeuThrArgAsnSerGlnProPheLys 487

Qy 1244 -----------------------CCTGCTTCC- 1252
                               ||||||||:
Db  488 LeuAspAspProLysSerAlaHisArgLysValSerHisArgAspAsnLeuThrValGlu 507

Qy 1253 -----------------------------------------TCTCCAGAACCGTTTTCATCCATGCCACCT 1282
                                                 |:|||||| ||||||||||||||||||| |||
Db  508 ArgAspGluSerSerLysLysSerSerHisThrProGluArgPheThrSerGlnGlySer 527

Qy 1283 ---------------------GCTCGAGATGTCCTGTGACACAGGGG 1321
                             |||||||| ||::|||:||||||:||
Db  528 TyrGlyValAlaGlyAsnValPheIleAspSerAspSerGlyArgHisTyrArgTrpGluValIle 547

Qy 1322 AATTGGCCTCT 1354
        |:|||||:|:|
Db  548 SerGlySerThrTrpTyrAlaIleGlyLeuLeuAlaTyrLysSerAlaProLeuHisGlu 567

Qy 1355 TCAGGCCCTTCAGCAGCGGAAACTCGGGATCCCTTGTTTTTACCCTAGTTGGTATAAAGGC 1414
        :||||||::||:|||| |||  |::||: |||:||   ::||:| ::|||:: :||||||:
Db  568 IleGlyLysAsnSerAlaSerTrpAlaLeuAlaSerArgCysAsnAsnAsnTrpValValArg 587

Qy 1415 CAAAGCCGGAAAAACCAGCTCCAACCCACCTTGCACTCATGGGGTGAAGGTTCTCGGGTCAA 1474
        ||| |:||| ||||||| |:|: |:|  ::|| |||:||:|||  |:| ||:||:||||||
Db  588 HisAsnSerLysGlyIleLeuProIleGluProAlaProHis------LeuArgArg 603

Qy 1475 ATAGGGCCTCTG 1486
        |:|||||:|:||
Db  604 ValGlyIleLeu 607
```

RESULT 3

S28418

probable zinc-binding protein - Iberian ribbed newt
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28418; S29476
R;Bellini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A;Title: A putative zinc-binding protein on lampbrush chromosome loops.
A;Reference number: S28418; MUID:93154311; PMID:7679068
A;Accession: S28418

A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-624 <BEL>
A;Cross-references: UNIPROT:Q02084; EMBL:L04190
R;Bellini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29476
A;Accession: S29476
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Accession:
A;Residues: 1-263, 'LK', 266-624 <BE2>
A;Cross-references: EMBL:L04190; NID:g1213867; PID:g213868
A;Cross-references: EMBL:L04190; NID:g1213867; PID:g213868
C;Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells an
C;Superfamily: rfp transforming protein
C;Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F;158-207/Domain: RING finger homology <RNG>

Alignment Scores:
Pred. No.:
Score:　　　　　　　　　　2.95e-09
Score:　　　　　　　　　　259.00
Percent Similarity:　　　42.99%　　　Matches:　　　　78
Percent Similarity:　　　23.28%　　　Conservative:　66
Best Local Similarity:　5.62%　　　　Mismatches:　　119
Query Match:　　　　　　 2　　　　　　Indels:　　　　72
　　　　　　　　　　　　　　　　　　　Gaps:　　　　　15
Length:　　　　　　　　 624

US-10-775-627A-3 (1-2590) x S28418 (1-624)

Qy   56 CTCAGGACLAGGGACGCCAAGAAAATGAGCACTTCTCTGAATTACAAGTCTTTCCAA 115
                                                                  :::
Db   137 IleGluAspGlyAspGlyAspGlnIleuGlyLys   ArgLys 148

Qy   116 GAGCAGACGACCATTGAGATTAACTTGGAAAAAGCAACTGAATCTGTCCCATCTGCCTAGAGATG 175
          ||| ::: :::
Db   149 ValAspAspGluGluAspAspAspPheThrGluAspGluThrCysProLeuCysArgSerLeu   168

Qy   176 TTCACGAAGCCTGTGGTTCATTCTCCCTTGCCAGCACAACTGTGCAGAAATGCCAGT 235
          ||| ||| :::
Db   169 PheLysGluPro---ValIleLeuGluCysGlyHisAsnPheCysLysLysHisCysIleAsp   187

Qy   236 GACATCTTCAGGGCCTCTAACCGTACTTACCCACACAGAGGAGGAGCACCACCGTGGGCATCA 295
          :::::::
Db   188 LysSerTrpGlu---   Ser 192

Qy   296 GGGGGGCCGCTTCCGCTGGTCTCCTCTCCGAGACATGAGGTGGTGTTAGACAGACATGAAGGTC 355
          |||||||
Db   193 AlaSerAlaPheSerCysProGluCysLys--GluValLeuThrGluArgLys----   209

Qy   356 TATGGACTGCAGAGG----AACCTGCTCGTGGAAAACATTATTGATATTCTACAAG 406
                                                         ::: :::
Db   210 TyrThrThrAsnArgValLeuAlaAsnLeuValLysLysAlaValGlyVal---Lys 228

Qy   407 CAGGAATCCCACAGGCCAGAAAAAAATTGGACCACCGCGTGTGAAAGACATAAAGAG 466
          |||
Db   229 AspLysAspValLysProLeuGlyLys   CysAspGluHis---Asp 242

Qy   467 GAACGGCATCAACATCTATTGTCTGAACGTGCCACCTGTTCCTGTGCAAGGTT 526
          ||||| |||
Db   243 GluArgHisLysLeuPheCysGlyAspGlyThrLeuIleAlaCysValIleCysArgAsp 262

Qy   527 TTTGGGCCCCATAAGGACTGCCAGGTGGCTCCCCTGACTCATGTGTTCAGAGGCGAAG 586
          ||||| |||
Db   263 SerLysGlyLeuHisSerAsnHisPheLeuPro   273

Qy   587 TCAGAGCTCAGTGATGGTATTGTCTTGTGGAAGCAACGAAGTCCAGGGGTGTG 646
          :::
Db   274 ----IleGlnAspAlaValGlyValTyr------ArgAspGlnLeuIleAlaLeu 288

Qy   647 ATCAGCCAGCTGGAGGAGAGACACCTGTAAAACTATTAGAG----   700
          ||| :::
Db   289 ValSerProLeuGluThrThrMetLysGluLysGlyLeuLysCysAspGlnSerGln 308

Qy   701 AAACAGGGACCTG-----   TGTGAGAAA 724
          ||| ||| :::||||
Db   309 LysIleSerLeuHisArgGluAsnIleValAspCysLysLysHisIleGluCysGluPhe 328

Qy   950 -------GCATCAAAAGGCCGTTTCAGAATGGAGAAAACTAGAACAAGGT 988
          ||||| :::::|| |||||
Db   409 ValProLeuAlaGluSerValLeuValAsnLysGluLeuSerGlnGly 423

RESULT 4
JC7562
glioblastoma RING finger protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7562
R;Vincent, S.R.; Kwasnicka, D.A.; Fretier, P.
Biochem. Biophys. Res. Commun. 279, 482-486, 2000
A;Title: A novel RING finger-B box-coiled-coil protein, GERP.
A;Reference number: JC7562; MUID: 20568703; PMID:1118312
A;Accession: JC7562
A;Molecule type: mRNA
A;Residues: 1-551 <VIN>
A;Cross-references: UNIPROT:Q9BZR9; GB:AF182046
C;Comment: This protein, a member of the RBCC subclass of RING finger proteins, is a tumo
A;Gene: gerp
A;Map position: 10q24.3
C;Genetics:
C;Keywords: coiled coil

Alignment Scores:
Pred. No.:
Score:　　　　　　　　　　7.21e-09
Score:　　　　　　　　　　253.00
Percent Similarity:　　　36.67%　　　Matches:　　　　101
Percent Similarity:　　　20.24%　　　Conservative:　82
Best Local Similarity:　5.49%　　　　Mismatches:　　186
Query Match:　　　　　　 2　　　　　　Indels:　　　　130
　　　　　　　　　　　　　　　　　　　Gaps:　　　　　18
Length:　　　　　　　　 551

US-10-775-627A-3 (1-2590) x JC7562 (1-551)

Qy   140 GAAAAAGCAACTGAATCTGTCCCATCTGCCTAGAGATGTTCACGAAGCCTGTGGTCATTCTC 199
          |||||:::||||| :::|| |||||
Db   10 GluGluGluLeuIleCysProIleCysLeuGluHisLeuValPheValGln--Leu 28

Qy   200 CCTTGCCAGCCACAACCTGTTGCAGGAAATGTGCCAGTGACATCTTCAGGGCCTCTAACCG 259
          ||||| ||| |||||
Db   29 ProCysGlyHisSerAsnPheCysAlaGlyCysIle-   39

Qy   260 TACTTACCCACAGGCCGGCACCACCGTGCCATCAGGGGGCGGCGTTCCGGTGTCCTCC 319
          |||
Db   40 -----GlyValAlaTrpAlaSerSerGlyLeuValAlaCysProGlu 54

Qy   320 TGCAGACATGAGGTGGTGTTAGACAGACATGGGGGTGTCTAT 367
          |||||:::||||| |||||
Db   55 CysAsnGln   AlaTyrAsnGlnLysProGlyLeuGlu 66

Qy   368 AGGAACCTGCTCGTGGAAAACATTATTGATATTCTAC------   403
          ||||| |||||
Db   67 LysAsnLeuLysLeuThrAsnIleValGlyLysPheAsnAlaLeuHisIleValGlyLysPro 86

Qy   404 -----   AAGCAGGAATCCCACAGGCCAGAAAAAAATTG 436
                                                        ||| :::|| :::

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: June 15, 2005, 02:24:18 ; Search time 235 Seconds
(without alignments)
11287.533 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 ctccgagattacccttacag..........ctccttccttcttcttccctcc 2590

Scoring table:
BLOSUM62

Xgapop	10.0 ;	Xgapext	0.5	
Ygapop	10.0 ;	Ygapext	0.5	
Fgapop	6.0 ;	Fgapext	7.0	
Delop	6.0 ;	Delext	7.0	

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum Match 100%

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn1_1/USPTO_spool_p/US10775627/runat_14062005_140909_19280/app_query.fasta_1.2759
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LCQPCL=0 -LCQPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10775627 @CGN_1_1_253 @runat_14062005_140909_19280 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
1:    uniprot_sprot:*
2:    uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2346.5	50.9	548	2	Q96DV2	homo sapien
2	2285.5	49.6	532	2	Q9BYV5	homo sapien
3	2232.5	48.4	540	2	Q8IUD9	homo sapien
4	1909.5	41.4	452	2	Q96DV3	homo sapien
5	1848.5	40.1	436	1	RN29_HUMAN	homo sapien
6	1239.5	26.9	360	2	Q6INV6	xenopus lae
7	1226	26.6	443	2	Q6DHS0	brachydanio
8	1162	25.2	366	2	Q9ERP3	mus musculu
9	1161	25.2	225	2	Q9GMX4	macaca fasc
10	1154	25.0	342	2	Q9BYV3	homo sapien
11	1126	24.4	384	2	Q9BYV2	homo sapien
12	1121	24.3	351	2	Q91Z63	rattus norv
13	1088.5	23.6	353	1	RN28_HUMAN	homo sapien
14	1077	23.4	346	2	Q6NR77	homo sapien
15	1063	23.1	241	2	Q8IUE4	homo sapien
16	1059	23.0	197	2	Q8C6Y1	mus musculu

ALIGNMENTS

17	1034.5	22.4	356	2	Q6DE39	xenopus lae
18	934.5	20.3	429	2	Q6DC78	brachydanio
19	910.5	19.7	345	2	Q6IQH8	brachydanio
20	861.5	18.7	348	2	Q7ZWH0	brachydanio
21	470.5	10.2	151	2	Q8BWC4	mus musculu
22	467.5	10.1	729	2	Q7TNM1	mus musculu
23	465	10.1	728	2	Q9NQ86	homo sapien
24	459.5	10.0	733	2	Q6NU77	xenopus lae
25	458	9.9	693	2	Q6PH04	brachydanio
26	440.5	9.6	729	2	Q80WG7	mus musculu
27	440	9.5	667	1	MID1_HUMAN	homo sapien
28	439.5	9.5	680	1	MID1_MOUSE	mus musculu
29	437.5	9.5	667	2	Q90WD1	gallus gall
30	437	9.5	668	2	Q6DEU6	xenopus tro
31	436	9.5	667	1	O15344	homo sapien
32	433.5	9.4	667	1	Q71R46	gallus gall
33	431	9.3	685	1	MID2_MOUSE	mus musculu
34	431	9.3	685	2	Q6GX19	acus trivi
35	431	9.3	685	2	Q6GX20	cercopithec
36	431	9.3	715	1	MID2_HUMAN	homo sapien
37	431	9.3	715	2	Q9UJV3	homo sapien
38	430	9.3	715	2	Q6GX21	cercopithec
39	423.5	9.2	759	2	MID1_MUSSP	mus spretus
40	421	9.1	441	2	Q7TNM2	mus musculu
41	420	9.1	524	2	Q641M2	mus musculu
42	414.5	9.0	424	2	Q6ZRL7	homo sapien
43	414	9.0	498	2	Q6P119	mus musculu
44	414	9.0	551	2	Q6NT17	homo sapien
45	413	9.0	759	2	Q7Z4K8	homo sapien

RESULT 1
Q96DV2

ID	Q96DV2
AC	Q96DV2;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	RING finger protein 29.
GN	Name=RNF29;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Cardiac muscle;
RX	MEDLINE=22302063; PubMed=12414993;
RA	Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
RA	Fürst D.O., Karsenti E., Gautel M.;
RT	"Transient association of titin and myosin with microtubules in
RT	nascent myofibrils directed by the MURF2 RING-finger protein.";
RL	J. Cell Sci. 115:4469-4482(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Cardiac muscle;
RA	Gautel M.S.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.
DR	EMBL; AJ243489; CAC43020.1; -.
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR	GO; GO:0008270; F:zinc ion binding; IEA.
DR	GO; GO:0016567; P:protein ubiquitination; IEA.

PRELIMINARY;   PRT;   548 AA.

RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac muscle;
RA Iakovenko A., Gautel M.;
RT "Titin-associated zinc-finger proteins link titin kinase to
RT transcriptional control.";
RL J. Muscle Res. Cell Motil. 21:833-833(2000).

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DR   InterPro; IPR000315; Znf_Bbox.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00643; zf-B_box; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00336; BBOX; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00119; ZF_BBOX; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50119; ZF_RING_2; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE 548 AA; 60465 MW; D7A5530A359FD67D CRC64;
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US-10-775-627A-3 (1-2590) x Q96DV2 (1-548)

Alignment Scores:

```
Pred. No.:           1.
Score:               1.77e-130
Score:               2346.50
Percent Similarity:  90.20%
Best Local Similarity: 84.03%
Query Match:         50.89%
DB:                  2
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Length: 548
Matches: 463
Conservative: 34
Mismatches: 46
Indels: 9
Gaps: 3

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Qy    80 ATGAGCAACTTCTCTGAATTACAAGGTCTTCTTCCAAAGACGACCACCATGGATAACTTG 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnThrThrMetAspAsnLeu  20

Qy   140 GAAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCAGGAGCCTGTGGTTCATTCTC 199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValValLeuLeu  40

Qy   200 CCTTGCCAGCAACCTGTGCAGGAAAAGTGCCAGTGAGCATCTTCCAGGGCCTCTAACCCG 259
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ProCysGlnHisAsnLeuCysArgGlyCysAlaSerAspIlePheGlnAlaSerAsnPro  60

Qy   260 TACTTACCCACAAGAGAGGAGCACCCGGTGGCATCAGGGAGCCGCGCTTCCGCTGTCCTCC 319
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TyrLeuProThrArgGluHisThrMetAlaSerGlyGlyArgPheArgCysProSer   80

Qy   320 TGCAGACATGAAGGTGGTGTTAGACAGGATGTCCTAGACTGGACAGAGGGAAACTTGCTC 379
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu 100

Qy   380 GTGGGAAAACATTATTGAATACTACAAGCGGGAATCACCCAGGCCCAGAAAAAAATGGAC 439
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 ValGlyAsnIleIleAspIleTyrLysGlnGluSerThrArgProGlyLysLysSerAsp 120

Qy   440 CAGCCCATGTGTGAACAGCATGAAGAGGAACGCCATCAACACTCTATTGTCTGAACTTGAA 499
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GlnProMetCysGluGlnHisGluGluArgHisIleAsnThrLeuIleTyrCysLeuGlu 140

Qy   500 GTGCCCACCTGTTCCTTGTGTCCAAGGTTTTTGGGCGCCCATAAGGACTGCTGCCAGGTCTCC 559
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Db   141 ValProThrCysSerLeuCysProLysValPheGlyAlaHisLysAspCysGlnValAlaPro 160

Qy   560 CTGACTCATGTGTTCCAGAGGGGTGTCATCAGCCAGCTGAGGGACACCTGTAAAACTATT 619
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 LeuThrHisValPheGlnArgGlyValIleSerGlnLeuArgAspThrCysLysThrIle 180

Qy   620 GGAAGCAACGATAGAGTCCAGGGTGTGTCATCAGCCAGCTGAGGGACACCTGTAAAACTATT 679
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuLeuGluAspThrCysLysThrIle 200
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RESULT 2
Q9BYV5

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Qy  1684 SerPheSerTrp-LeuAsnSerLeuAsnGlu 1714
         ||||||||||   ||||||||||||||||||
Db   539 GlnAlaLeuAlaAlaProAlaSerGlySerGlyAlaAspSerGluProAlaArgHisIlePhe 548
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21140140; PubMed=11243782; DOI=10.1006/jmbi.2001.4448;
RA   Centner T., Yano J., Kimura E., McElhinny A.S., Pelin K., Witt C.C.,
RA   Bang M.L., Trombitas K., Granzier H., Gregorio C.C., Sorimachi H.,
RA   Labeit S.;
RT   "Identification of muscle specific ring finger proteins as potential
RT   regulators of the titin kinase domain.";
RL   J. Mol. Biol. 306:717-726(2001).
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR   EMBL; AJ291712; CAC32840.1; -.
DR   GO; GO:0005874; C:microtubule; NAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR000315; Znf_Bbox.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00643; zf-B_box; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00336; BBOX; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50119; ZF_BBOX; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   532 AA;  58634 MW;  8F12BAD335558952 CRC64;

Alignment Scores:
Pred. No.:                    1

Score:                  7.14e-127
Score:                   2285.50
Percent Similarity:       90.47%
Best Local Similarity:    84.11%
Query Match:              49.57%
DB:                           2

Best Match:  US-10-775-627A-3 (1-2590) x Q9BYV5 (1-532)
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Qy    128 ATGGATAACTTGGAAAAAGCAAACTGAATCTGTTCCTAGAGATGTTCACGAGAAGCCT 187
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Db      1 ATGGATAACTTGGAAAAAGCAAACTGAATCTGTTCCTAGAGATGTTCACGAGAAGCCT 187

Qy      1 MetAspAsnLeuGluLysAlaAsnCysGluSerValProArgAspValHisGluLysPro 20
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Qy    188 GTGGTCATCTCCCTTGCCAGCACAACCCTGTGCAGTGACACTTTCCAG 247
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Db     21 ValValIleLeuProCysSerGlnHisSerAsnLeuCysSerArgLysCysAlaSerGlyLeuGlu 40

Qy    248 GCCTCTAACCCGTACTTACCCACAAGAGAGGAGGCCACCGTGTGCGAGCATCCAGGGGCGCTTC 307
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Db     41 AlaSerAsnProTyrLeuProThrArgGluGlyThrThrMetAlaSerGlyGlyArgPhe 60

Qy    308 CGCTGTCCCTCCTGCAGACATGAGGTGGTTGTAGACAGACAGGAGTGTTGAGACTGCAG 367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ArgCysProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGln 80

Qy    368 AGGAACCTCGTGGAAAAACATTATTGATATCTACAACCAGAGAATCACCAGGCCCAGA 427
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Qy    428 AAAAAATTGGAACAGCCCATGTGTCTGAAGAGAGCATCGAAGAGAGGACCATCAACATCTATTGT 487
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Db    101 LysLysLeuGluGlnProMetCysGluLysArgSerGluGlnIleAsnIleTyrCys 120

Qy    488 CTGAACTGTGAAGTGCCCACCTGTTCCTGTGCAAAGGTTTTGGCGCCATAAGGACTGC 547
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LeuAsnCysGluValProThrCysSerCysValPheGlyAlaHisLysAspCys 140

Qy    548 CAGGTGGCTCCCCTGACTCATGTGTTCTTCCAGAGGCAGAAGCTCAGTGATGGTATT 607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GlnValAlaProLeuThrHisValPheGlnArgGlnLysLeuSerAspGlyIle 160

Qy    608 GCTGTCACTTTGTGGGGGAGCAAGCAGACGATAGAGTCAGCCAGCGTGAGGACACC 667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 AlaIleLeuValGlySerAsnAspArgValGlnIleValIleSerGlnLeuGluAspThr 180

Qy    668 TGTAAAACTATTGAGGAGTGCTGCAGAAAGCAGAAACAGACACTTGTGTGAGAANTTTGAT 727
          |||||||||||||||||||||||||||||||||||||||||||||||||||::|||||||
Db    181 CysLysThrIleGluGluCysCysArgLysGlnLysGlnThrLeuValGluLysPheAsp 200

Qy    728 CACCTTATACGGCCATCCTGAGGAGGAGACTGAAATGACCAAGACCATCACTCGAACA 787
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Db    201 TyrLeuTyrGlyIleLeuGluGlyLysGlyAsnGluMetThrGlnValIleThrArgThr 220

Qy    848 AACCTATCCAAGTTGGGTGCAGTGCAGGAAATCCAGTTCATGGAGCCCAAATGGCAGTA 907
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Db    221 GlnGluGlyLeuGluGluHisValArgAlaLeuGluLysLysTyrSerAspHisGluGlu 240

Qy    908 TTTCTGCGAGAATGCCAAGGACCCTGTTGCAAAAGATCGTGGGGGAAGCCGTCAAAAGGCCTTTCAG 967
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Db    241 AsnValSerLysLeuValGlyIleGlnPheGlnMetGluProGluMetAlaVal 260

Qy   1028 GAAGAAAAAAATTATCCGTGAAATTGACTTTCTAGA 1081
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Qy    968 ATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTGCAATCTCAATGA 1027
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Db    281 MetGluLysLeuIleGluHisGlyTyrGluAsnMetAsnHisProThrValAsnLeuAsnArg 300

Qy   1082 GATGCCAGGAGAAATAGATGAAGAGGAGGAGGAGG 1132
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Db    301 GluValLeuIleLeuArgGluIleAspPheProTyrArgGluAspGluGluGlu 320

Qy   1133 GAAGAGGGCAGAAAAATGTTCAAATAGCCATCTTCAGGGGAGGAGGAGAGGAGTCTGGAAAGCT 1192
          ||||||||||||||::||||||||||||||||||||||||||||||||||||||||||||
Db    321 GluGlyGlyGluGlyGlyValGluGlyValGlyGlyGlyValGluValGluGluVal 340

Qy   1193 GCAGAGCCCTCTCAGCTTCCCGCAGCGCTTCAGTGGCGCCCGAGCCCACTACCTGCTTCC 1252
          ::::      |||||||||||||||||||||||||||||||||||||||||||
Db    341 GluGlyValGluGlyAsnValGlnThrGluPheProGlyGluAsnProGluGluLysSerAla 360

Qy   1253 TCTCCAGAACCGTTTTCATTCCATGCCACCTGCCAGGATGTCCTGGTGACACAGGGGGGAG 1312
          ||||||||||||||||||||||||||||||||::||||||||||||||||||||||||
Db    361 SerGluLeuSerGlnVal------GluLeuGlnAlaLeuAlaProGlyAlaLeuProValSer 378

Qy   1313 GTGGTGCCCATTGGCTCCAGACAGCCACACAGTCTGAAACTTCAGGCCCTTCAGCGCG 1372
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Qy   1433 TCCAACCCACCTTGCCACTCCATGGGAGTGAAGGTCGGGCTCGGGAACTAGGGGCCATT 1492
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Db    439 ThrAsnProProCysThrProCysSerGluGluProTrpTyrTyrLysGlyGlnThrArg 438

Qy   1373 GAAACTGCGGATCCCCTGTTTTACCCTAGTTGGTATAAAGGCCAAAGCCGGAAAACCAGC 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||    :::
Db    419 GluThrAlaAspProLeuPheTyrProSerTrpTyrLysGlyGlnThrArgLysAlaThr 438

Qy   1493 GAGGATTCCAGTGTGTCCGCAGAAGTCGCAGAAGCCCACCAAATGAGACGGACAGCA 1552
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Db    439 ThrAsnProProCysThrProCysSerGluGluProTrpTyrTyrLysGlyGlnThrArg 458

Qy   1553 GTGAGGTGGTAAGAGTCTAGTTGTTCAACTGGAGACCTCTCCAGATTTGGGATTTGAGG 1612
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Qy   1613 TCTCCCAGGGACAGTCTGCCAGCCCCTTGGGGGGTGGGGGT-GATCCTGAGGGCCAGCT 1671
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Db    479 ValSerGlyValSerGluThrSerAlaAlaProAlaAlaThrSerGlnIleGlyPheGluAlaPro 498

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Db    499 ProLeuGlnGlyGlnAlaAlaAlaProAlaAlaSerAspSerGluProAla 518

Db    519 ArgHisIlePheSerPheSerTrp-LeuAsnSerLeuAsnGlu 532
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ID   Q8IUD9              PRELIMINARY;    PRT;   540 AA.
AC   Q8IUD9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   RING finger protein 29.
GN   Name=RNF29;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Iakovenko A., Gautel M.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=22302063; PubMed=12414993;
RA   Pizon V., Iakovenko A., Van der Ven P.F.M., Kelly R.A., Fatu C.,
RA   Furst D.O., Karsenti E., Gautel M.;
RT   "Transient association of titin and myosin with microtubules in
RT   nascent myofibrils directed by the MURF2 RING-finger protein.";
RL   J. Cell Sci. 115:4469-4482(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Gautel M.S.;
RT   "Titin-associated zinc-finger proteins link titin kinase to
RT   transcriptional control.";
RL   J. Muscle Res. Cell Motil. 21:833-833(2000).
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR   EMBL; AJ431704; CAD24432.1; -.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR000315; Znf_Bbox.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00643; zf-B_box; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00336; BBOX; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50119; ZF_BBOX; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   540 AA;  60245 MW;  D16B7E706BF9C60A CRC64;
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US-10-775-627A-3 (1-2590) x Q8IUD9 (1-540)

Alignment Scores:

Pred. No.:	9.72e-124
Score:	2232.50
Percent Similarity:	91.18%
Best Local Similarity:	84.90%
Query Match:	48.42%
DB:	

Length:	540
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Conservative:	32
Mismatches:	38
Indels:	7
Gaps:	3

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Qy    200 CCTTGCCAGACAACCTGTGGCAGGGAAAATGTGCCAGTGACATCTTCCAGGCCCTTCTAACCCG  259
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Qy    320 TGCAGACATGAGGTGGTGTTAGACAGACATGGGATGGGTCTATGACTGCAGAGGAACCTGCTC  379
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Qy    440 CAGCCCATGTGTGAAGACATGAAGAGGAGGCCATCAACATCTATTGTCTGAAACTGTGAA  499
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Qy    500 GTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCCATAAGGACTTGCCCC  559
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Qy    620 GGAAGCAACGATGAGTCCAGGGTGTGATCAGCAGCGTGACACCTGGAGGAGACACCTGTAAAACTATT  679
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Qy    680 GAGGAGTGGCTGCAGAAAAGCAGAAAACAGGACCTGTGTGTGAGAAATTTGATCACCTATACGGC  739
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Qy    740 ATCCTTGGAGGGAGAAGAATCCCAAGCCCATCATCTCGAACACAGGAGGAGAA  799
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Qy    800 CTGGAACATGTCCGAACTCTTATCACGAAGAAGTTGCAGGAAGAGTCATCCAAG  859
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Qy    920 GCCAAGACCCTGTTCAAAAAGAATCGTTGGAAGCAATCAAAAGGCGTTCAGATGGAGAACTA  979
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Qy    980 GAACAAGGTTATGAGATCACATGAGCCAACTTCACTCGTCAAATCCAATAGAAGAGAAAAATT  1039
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Qy   1088 GGAGAAATAGATGAAGAGAAGAGAGAA----GGAGAGGATGCACGAGAAGTCAGTAGAAGAGGCAGAA  1144
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Qy   1145 AATGTTCAAATAGCATCTTCAGGGGGAAGAGGAGTCTGAGAACGTTCAGCAGCCCTCT  1204
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Qy   1205 CAGCTTCCGCGAGAGCTTCAGTCGCCCCAGAGCCACTACCTGCTTCTCCCAGAACCG  1264
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Qy   1265 TTTTCATCCATGCCACCTGCTGCGACGATGTCCTGGTGCACACAGGGGGAGGTGCCCATT  1324
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Qy   1325 GGCTCTCAGAGACCACAGTCTGAAACTTCAGCGCGAAACTGCGGAT  1384
Db
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OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: June 15, 2005, 06:22:55 ; Search time 46 Seconds
                                                  (without alignments)
                                                  8406.134 Million cell updates/sec

Title: US-10-775-627A-3
Perfect score: 4611
Sequence: 1 ctcgagattacccttacag............ctccttccttcttccctcc 2590

Scoring table: BLOSUM62
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                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 513545 seqs, 74649064 residues

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters: -DEV=xlp
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10775627 @CGN_1_1_35 @runat_14062005_140910_19310 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2809	60.9	545	4	US-09-908-988B-4	Sequence 4, Appli
2	1162	25.2	366	4	US-09-908-988B-2	Sequence 2, Appli
3	1088.5	23.6	353	4	US-09-484-970B-171	Sequence 171, App
4	1082	23.5	343	4	US-09-908-988B-6	Sequence 6, Appli
5	232.5	5.0	223	4	US-09-327-983-5	Sequence 5, Appli
6	228.5	5.0	539	4	US-09-949-016-6363	Sequence 6363, Ap
7	226.5	4.9	842	4	US-09-949-016-7012	Sequence 7012, Ap
8	226.5	4.9	870	4	US-09-949-016-9625	Sequence 9625, Ap
9	223.5	4.8	435	4	US-09-561-989-10	Sequence 10, Appl
10	223	4.8	519	4	US-09-949-016-7883	Sequence 7883, Ap
11	216.5	4.7	413	4	US-09-663-600A-198	Sequence 198, App
12	213.5	4.6	513	4	US-09-949-016-10972	Sequence 10972, A
13	207	4.5	487	2	US-08-724-394A-7	Sequence 7, Appli
14	206	4.5	475	4	US-09-949-016-6317	Sequence 6317, Ap
15	206	4.5	487	4	US-09-949-016-11205	Sequence 11205, A
16	204	4.4	643	4	US-09-949-016-10023	Sequence 10023, A
17	199.5	4.3	327	4	US-09-949-016-7575	Sequence 7575, Ap
18	199	4.3	835	4	US-09-949-016-9685	Sequence 9685, Ap
19	194	4.2	447	4	US-09-949-016-7884	Sequence 7884, Ap
20	187	4.1	218	4	US-09-327-983-6	Sequence 6, Appli
21	183.5	4.0	485	2	US-08-724-394A-8	Sequence 8, Appli
22	174	3.8	1155	4	US-09-949-016-10125	Sequence 10125, A
23	174	3.8	1155	4	US-09-949-016-10126	Sequence 10126, A
24	173.5	3.8	717	3	US-08-910-925-1	Sequence 1, Appli
25	172.5	3.7	574	1	US-08-049-473-2	Sequence 2, Appli
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27	172.5	3.7	574	4	US-08-921-099A-7	Sequence 7, Appli
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29	172.5	3.7	581	4	US-09-949-016-11632	Sequence 11632, A
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ALIGNMENTS

RESULT 1
US-09-908-988B-4

; Sequence 4, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 545
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-908-988B-4

Alignment Scores:
Pred. No.:   1.1e-255
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.92%

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Gaps:	0	

US-10-775-627A-3 (1-2590) x US-09-908-988B-4 (1-545)

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(Sequence alignment — Qy/Db rows, read vertically)

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Qy   260  TACTTACCCACCAAGAGAGAGAGGACCACACCGTGCCATCAGCGGGCGCCGCTTCCGTGTCCCTCC  319
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Qy   440  CAGCCCATGTGTGAAGACAGCATGAGAGCCATCAAACATCTATTGTCTGAACTGTGAA  499
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Qy   740  ATCCTGGAGAGGAAGCAATCAAATAACCCAAGCCATCACTCGACACACAGGAGGAGAAA  799
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Db   301  GluGlnGlyTyrGluIleMetSerAsnPheThrValAsnLeuAsnArgGluGluLysIle  320

Qy  1040  ATCCGTGAAAATTGACTTTTCTAGAGGAAGAGAAGCTGCAGGAGGAAGAGAAATAGAT  1099
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Qy  1160  TCTTCAGGGGAGGAGGAGAGTCTGGAGAAAGCTGCAGAGGAGGAAGAGAAGAG  1219
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Pred. No.:	
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Score:	1162.00
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Percent Similarity:	76.99%
	Conservative: 55
Best Local Similarity:	61.92%
	Mismatches: 76
Query Match:	25.20%
	Indels: 8
	Gaps: 4
DB:	

US-10-775-627A-3 (1-2590) x US-09-908-988B-2 (1-366)

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Qy    80  ATGAGACACTTCTCTGAATTACACAGTCTTTCTCCAAAGACAGCAGCAGACCATGATAACTTG  139
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US-09-484-970B-171
; Sequence 171, Application US/09484970B
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; Patent No. 6426186
; GENERAL INFORMATION:
;  APPLICANT: Jones, Karen A.
;  APPLICANT: Volkmuth, Wayne
;  APPLICANT: Walker, Michael G.
;  TITLE OF INVENTION: BONE REMODELING GENES
;  FILE REFERENCE: PB-0014 US
;  CURRENT APPLICATION NUMBER: US/09/484,970B
;  CURRENT FILING DATE: 2000-01-18
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: PERL Program
; SEQ ID NO 171
;  LENGTH: 353
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No. 6426186 3575519CD1 (GENE ID 247384)
US-09-484-970B-171
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Pred. No.:
Score:                        1088.50
Percent Similarity:   72.19%
Best Local Similarity: 57.22%
Query Match:          23.61%
DB:
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US-10-775-627A-3 (1-2590) x US-09-484-970B-171 (1-353)

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Qy   209 CACAACCTGTGCAGGGAAAATGTGCCAGTGACATCTTCCAGGGCCTCTAACCCGTTACTTACC 268
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Qy   269 ACAAGAGGAGGAGCACCACCGTGGCATCAGGGGGCGCCCTTCCGCTGTCCCTGCGACAT 328
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Qy   626 AACGATAGAGTCCAGGGTGTGATCAGCCCAACTGCAGGACACCTGTAAAACTATTAGGAG 685
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RESULT 4
US-09-908-988B-6
; Sequence 6, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-908-988B-6

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Pred. No.:
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Query Match: 63.58%
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US-10-775-627A-3 (1-2590) x US-09-908-988B-6 (1-343)

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Db   21 LeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeuProCysGln 40

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
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Run on: June 15, 2005, 08:08:44 ; Search time 692.5 Seconds
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query % Match	Length	DB ID	Description
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2	2809	60.9	545	16	US-10-775-649-4	Sequence 4, Appli
3	2809	60.9	545	16	US-10-775-627-4	Sequence 4, Appli
4	2359.5	51.2	548	15	US-10-104-047-2643	Sequence 2643, Ap
5	1922.5	41.7	452	15	US-10-104-047-2403	Sequence 2403, Ap
6	1922.5	41.7	452	16	US-10-473-574-8	Sequence 8, Appli
7	1735.5	37.6	414	9	US-09-764-864-821	Sequence 821, Appl
8	1166	25.3	358	10	US-09-908-988B-58	Sequence 58, Appl
9	1162	25.2	366	9	US-09-908-988B-2	Sequence 2, Appli
10	1162	25.2	366	16	US-10-775-649-2	Sequence 2, Appli
11	1162	25.2	366	16	US-10-775-627-2	Sequence 2, Appli
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17	1121	24.3	351	14	US-10-061-043A-45	Sequence 45, Appl
18	1121	24.3	351	14	US-10-061-043A-46	Sequence 46, Appl
19	1121	24.3	351	14	US-10-061-043A-47	Sequence 47, Appl
20	1121	24.3	351	15	US-10-060-634C-21	Sequence 21, Appl
21	1121	24.3	351	15	US-10-060-634C-36	Sequence 36, Appl
22	1121	24.3	351	15	US-10-060-634C-45	Sequence 45, Appl
23	1121	24.3	351	15	US-10-060-634C-46	Sequence 46, Appl
24	1121	24.3	351	15	US-10-060-634C-47	Sequence 47, Appl
25	1088.5	23.6	353	16	US-10-094-749-2861	Sequence 2861, Appl
26	1088.5	23.6	353	15	US-10-221-625-85	Sequence 85, Appl
27	1087.5	23.6	353	14	US-10-061-043A-48	Sequence 48, Appl
28	1087.5	23.6	353	15	US-10-060-634C-48	Sequence 48, Appl
29	1086	23.6	289	14	US-10-061-043A-39	Sequence 39, Appl
30	1086	23.6	289	15	US-10-060-634C-39	Sequence 39, Appl
31	1086	23.6	340	14	US-10-061-043A-23	Sequence 23, Appl
32	1086	23.6	340	15	US-10-060-634C-23	Sequence 23, Appl
33	1082.5	23.5	366	9	US-09-764-864-808	Sequence 808, Appl
34	1082	23.5	343	9	US-09-908-988B-6	Sequence 6, Appli
35	1082	23.5	343	16	US-10-775-649-6	Sequence 6, Appli
36	1082	23.5	343	16	US-10-775-627-6	Sequence 6, Appli
37	1022	22.2	326	15	US-10-250-613-4	Sequence 4, Appli
38	1022	22.2	202	14	US-10-061-043A-33	Sequence 33, Appl
39	790	17.1	202	15	US-10-060-634C-33	Sequence 33, Appl
40	786	17.0	184	9	US-09-764-864-1280	Sequence 1280, Ap
41	634.5	13.8	143	11	US-09-864-408A-6102	Sequence 6102, Ap
42	436	9.5	667	16	US-10-723-860-4278	Sequence 4278, Ap
43	432.5	9.4	552	16	US-10-408-765A-2368	Sequence 2368, Ap
44	405	8.8	736	15	US-10-108-260A-3552	Sequence 3552, Ap
45	387	8.4	122	9	US-09-764-864-1269	Sequence 1269, Ap

ALIGNMENTS

RESULT 1
US-09-908-988B-4
Sequence 4, Application US/09908988B
Patent No. US2002012769OA1
GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 545
TYPE: PRT
ORGANISM: Mus musculus

US-09-908-988B-4

Alignment Scores:

Pred. No.:
Score: 2809.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.92%
DB: 9

Length: 545
Matches: 545
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-775-627A-3 (1-2590) x US-09-908-988B-4 (1-545)

Qy	80	ATGAGGACTTCTCTGAATTACAAGTCTTTCTTCCAAAGAGCAGCAGACCATGGATAACTTG	139
Db	1	MetSerThrSerLeuAsnTyrLysSerPheSerLysGluGlnGlnThrMetAspAsnLeu	20

| Qy | 140 | GAAAAGCAACTGATCTCTTCCATCTGCTAGAGATGTTCACCGAAGCCTGTGGTCATTCTC | 199 |
| Db | 21 | GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeu | 40 |

| Qy | 200 | CCTTGCCAGCACAACCTGTGCAGGAAATGTCCCAGTGACACTCTTTCCAGGCCTCTAACCCG | 259 |
| Db | 41 | ProCysGlnHisAsnLeuCysArgLysCysLeuProGlnAlaSerAsnProPro | 60 |

| Qy | 260 | TACTTACCCACAAGAGGAGGCCACCGTGGCCATGGGGCGCCGTTCCGTGTCCCTCC | 319 |
| Db | 61 | TyrLeuProThrArgGlyGlyThrValAlaSerGlyArgArgPheArgCysProSer | 80 |

| Qy | 320 | TGCAGACATGAGGTGGTGTTAGACAGAGACCTGGGGGTCTTATGGACTGCAGAGACCTGCTC | 379 |
| Db | 81 | CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu | 100 |

| Qy | 380 | GTGGAAAAACATATTATTGATATCTTACACAGCCAGAGAATCCACCGGCCACGAAAAAATTGGAC | 439 |
| Db | 101 | ValGluAsnIleIleAspIleLeuHisSerGlnArgIleHisArgProArgLysLysLeuAsp | 120 |

| Qy | 440 | CAGCCCCATGTCTGTTCCTTGTGCAAAGGTTTTTGGCGCCCATAGAACTCCCAGGTGGCCTCCC | 499 |
| Db | 121 | GlnProMetCysSerLeuCysLysGlyLeuTrpArgProIleGluLeuProGlyGlyPro | 140 |

| Qy | 500 | GTGGCCACCTGTTCCTTGTGCAAAGGTTTTTGGCGCCCATAGAACTCCCAGGTGGCCTCCC | 559 |
| Db | 141 | ValProThrCysSerLeuCysLysValPheHisGlyAlaHisLysAspCysGlnValAlaPro | 160 |

| Qy | 560 | CTGACTCATGTGTTCCAGAGCCAGAGAGTCACAGCTCAGTGAATGGTAATTGCGTACTTGTG | 619 |
| Db | 161 | LeuThrHisValPheGlnSerGlnArgValThrAlaGlnLeuSerGlyIleAlaValLeuVal | 180 |

| Qy | 620 | GGAAGCAACGATAGAGCTTCCAGGGTGTGATCAGCCAGTGGGACCACCTGTAAAACTATT | 679 |
| Db | 181 | GlySerAsnAspArgValGlnGlyValIleSerGlnLeuGluAspThrCysLysLysThrIle | 200 |

| Qy | 740 | ATCCTCGGAGAGAGGAGGACTGAAAATGACCCAAAGCCATCACTCACTGCGAGAGAA | 799 |
| Db | 221 | IleLeuGlyGluArgArgThrGluMetThrGlnSerHisSerLeuThrAlaGluGlyLys | 240 |

| Qy | 800 | CTGGAACATGTCCGAACTCTTTATCAGGAAGTATTCCGATCACCTGGGAGAACGTATCCAAG | 859 |
| Db | 241 | LeuGluHisValArgThrLeuTyrGlnGluValPheArgSerProGlyGluArgIleGlnLys | 260 |

| Qy | 860 | TTGGGTGGATGCAGGAATCCAGTTCATCGAGTGTGAGCCCGGGGTATTTCTGCAGAAT | 919 |
| Db | 261 | LeuValGlySerGlyIleGlnPheHisGluCysGluProGlyValPheLeuGlnAsn | 280 |

| Qy | 920 | GCCAAGAGACCCCTGTTGGGAAAAGATCGTGGGAAAAGGGGGTTTCAAAAGGAGAAACTA | 979 |
| Db | 281 | AlaLysArgProLeuLeuGlyLysIleValGlyLysAlaSerLysAlaPheGlnMetGluLysLeu | 300 |

| Qy | 980 | GAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCAATACGAGAGAGAAAAATT | 1039 |

US-10-775-627A-3 (1-2590) x US-09-908-988B-4 (1-545)

| Db | 301 | GluIleGlnGlyTyrGluIleMetSerAsnPheThrValAsnLeuAsnArgGluArgGluLysIle | 320 |

| Qy | 1040 | ATCCGTGAAAATTGACTTTTCTAGAGAAGGAGAAGGAGATCCAGAAGAAATAGAT | 1099 |
| Db | 321 | IleArgGluIleAspPheSerArgGluGlyGluGlyGluGlyGluGluAspProGluGluIleAsp | 340 |

| Qy | 1100 | GAAGAAGGAGGAGGAGGATCCAGTAGAAGTAGAAGAGGCAGAAAATGTTCAAAATGCA | 1159 |
| Db | 341 | GluGluGlyGlyGlyGlyGlyGluAspProAlaValGluValGluGluAlaGluAsnValGlnAsnAlaIleAla | 360 |

| Qy | 1160 | TCTTCAGGGAAGAGAGAGAGTTCTGAGAAAGCTCGAGAAAAGCTGCAGAAGCCCTCTCAGAG | 1219 |
| Db | 361 | SerSerGlyGluGluGluGluSerLeuGluLysAlaAlaGluProSerGlnLeuProAlaGlu | 380 |

| Qy | 1220 | CTTCAGGTTCGCCCCAGCCACTACCTGCTTCCTCCTCCAGAGGCTGTTTCATCCATGCCA | 1279 |
| Db | 381 | LeuGlnValAlaProGluProLeuProAlaSerSerSerProGluProSerSerMetPro | 400 |

| Qy | 1280 | CCTGCTCCAGATGTCCTGGTGACACAGGGCGGACGAGGTGGTGCCCATTGGCTCTGCAGACC | 1339 |
| Db | 401 | ProAlaAlaAspValLeuValThrGlnGlyGlyArgGlyGlyAlaHisTrpLeuSerGlnThr | 420 |

| Qy | 1340 | ACACAGTCTGAAAACTTCAGGGCTCCTCAGCGCGGGAAAAACTGGGGATCCCTTGTTTTACCCT | 1399 |
| Db | 421 | ThrGlnSerGluThrSerGlyLeuProSerAlaAlaGlyGluThrAlaAlaAspProLeuPheTyrPro | 440 |

| Qy | 1400 | AGTTGGTTATAAAAGGCCAAAGGCCGGAAAACCAGCTCCAAACCACCTTGCACTCCATGGGAGT | 1459 |
| Db | 441 | SerTrpTyrLysGlyGlnSerArgLysThrSerSerAsnProProCysThrHisGlySer | 460 |

| Qy | 1460 | GAAGGTCTGGGTCAAATAGGGCGCCCTGGGCATTGAGGGATTCCAGTGTGCCAGTCCGCAGAA | 1519 |
| Db | 461 | GluGlyLeuGlyGlnIleGlyProLeuGlyIleGluGlyPheGlnSerValGlnSerArgAlaGlu | 480 |

| Qy | 1520 | GTGGCAGAAGGCCGCCAACCATGAGCAGAGGGCAGCAGTGAGTGTGAAGAGGAGCTGTTAGTTCAACT | 1579 |
| Db | 481 | ValAlaGluGlyArgGlnProMetSerArgGlyGlnGlnValSerValLysArgSerCysSerThr | 500 |

| Qy | 1580 | GCAGCTACCTCTCAGATTGGGATTGAGGCCGCCCCTCTCCCCAGGGGACAGTCTTGCAGCCTTG | 1639 |
| Db | 501 | AlaAlaThrSerGlnIleGlyIleGluProGluAlaProSerProGlyGlyGlnSerAlaAlaLeu | 520 |

| Qy | 1640 | GGGAGGTGGGGGTGGGGGTTGATCCTGAGCCAGTGCCAGCAGTGCTTCTCCTTCTCCTGGTTTG | 1699 |
| Db | 521 | GlySerGlyGlyGlyValIleLeuSerGlnLeuLeuAlaThrSerSerProSerProGlyLeu | 540 |

| Qy | 1700 | AATTCCCTAAATGAA | 1714 |
| Db | 541 | AsnSerLeuAsnGlu | 545 |

US-10-775-649-4

Alignment Scores:

Pred. No.:
Score: 3.45e-210
                                2809.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 60.92%

Length: 545
Matches: 545
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-775-627A-3 (1-2590) x US-10-775-649-4 (1-545)

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Qy    80 ATGAGCACTTCTCTGAAATTACAACTGTCTTTTCTCCAAAGACAGCAGCCATGGGATAAGTTG 139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetSerThrSerLeuAsnTyrLysSerPheSerLeuGlnGlnThrMetAspAsnLeu 20

Qy   140 GAAAAGCAAACTGATCTGTCCCATCTGGCCTAGAGATGTTCACGAAGCCTGGGTCATTCTC 199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValIleLeu 40

Qy   200 CCTTGCCCAGCACACCTGTCCAGGAAATGTCCAGTGACATCTTCCAGGCCTCTAACCCG 259
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro 60

Qy   260 TACTTACCCACAAGAGAGGAGGCACCACCCGTGGCATCAGGGCATCATGGGCCCCTTGCCCCTCC 319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TyrLeuProThrArgGlyGlyThrThrValAlaSerGlyIleArgAlaSerProSer 80

Qy   320 TGCACAATCAGGTGGTTGTTAGACTACAAGGGTCTAGGACTTCAGAGGAACCTGCTC 379
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 CysArgHisGlnValValLeuAspTyrLysGlyLeuGlyLeuGlnArgAsnLeuLeu 100

Qy   380 GTGGAAAACATTATTGATAACTACACAAGACAGGAATCCACCAGCCAGAAAAAATTGGAC 439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 ValGluAsnIleIleAspIleTyrLysGlnGluSerThrArgProGlyLysLysLeuAsp 120

Qy   440 CAGCCCCATGTGTGAAGAGCATGAAGAGCGCATCAACATCTATTGTTCTGAACTTGTGAA 499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GlnProMetCysGluGluHisGluGluArgIleAsnIleTyrCysLeuAsnCysGlu 140

Qy   500 GTGCCCACCTGTTCCTTGTGTCAAGGTTTTTGGCGCCCATAAGGACTGCCAGGTGGCTCCC 559
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 ValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGlnValAlaPro 160

Qy   560 CTGACTCATGTGTTCCAGAGACGGCAGAAGTCAGTCGAGTGTATTGCTGTACTTGTG 619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 LeuThrHisValPheGlnArgGlnLysSerGluSerAspGlyIleAlaValLeuVal 180

Qy   620 GGAAGCAACGATAGAGTCCAAGGGTGTGATCACCAGCCAGCCACCTGTAAAAACTATT 679
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuAspThrCysLysThrIle 200

Qy   680 GAGGAGTGCTGCAGAAACAGGAACAACAGGACCTGTGTGAGAAATTTGATCACCTATACGGC 739
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GluGluCysCysArgLysArgAsnAsnArgThrCysValArgAsnLeuIleThrTyrThr 220

Qy   740 ATCCTCGGAGGAGGAGGAGGACTGAAAATGACCCAAGCCATCTCGACACAGGAGGAGAA 799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 IleLeuGlyGlyGlyGlyLeuLysMetThrGlnAlaIleSerThrGlnGluGluLys 240

Qy   800 CTGGAACAGTCCGAACTCTTATCAGGAGTATTCCGATCACCTGGAGAACGGTATCCCAAG 859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LeuGluHisValAlaArgThrLeuIleArgGlyTyrSerAspHisLeuGluAsnValSerLys 260

Qy   860 TTGGTGGGAGTCAGGAATCCAGTTGTCATGGAGTGAGCCCGAACTGGCAGTATTTCTGCAGAAT 919
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 LeuValGluSerGlyIleGlnAsnPheMetAspGluProGluMetAlaValPheLeuGlnAsn 280

Qy   920 GCCAAGACCCGTGTTGCAAAAGAATCGTGGAACATCAAAAGGCGTTTCAGATGATGGAGAAACTA 979
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 AlaLysThrLeuLeuGlnLysIleValGluAlaSerLysAlaPheGlnMetGluGlyLysLeu 300

Qy   980 GAACAAGGTTATGAGAATCAAGCAACTTCACTGTCAATCTCAATAGAGGAGAGAAAAAATT 1039
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GluGlnGlyTyrGluIleMetSerAsnPheThrValAsnLeuAsnArgGluGlyLysIle 320

Qy  1040 ATCCCTGAAATTGACTTTTCTTAGAGAAGAGGAGAAGAGGAAGAGGAACAGCAGAAATAGAT 1099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 IleArgGluIleAspPheSerArgGluGluGluGluLysLysArgSerGlnGluAspAsp 340

Qy  1100 GAAGAAGGAGAAGGAGGAGCATGCAGTAGAAGAGCTAGAGAAGTAGAAGGAGAAAATGTTCAAATAGCA 1159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 GluGluGlyGluGlyGlyAlaGluGluAspSerSerGlyLysGlnThr 360
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(continued alignment)

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Qy  1160 TCTTCAGGGGAAGAGGAGGAGTCTGGAGAAAGCTGAGAGCCCTCTCAGGCTTCCCGGAG 1219
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SerSerGlyGluGluGluSerGlyGluSerLysAlaAspArgLeuProAlaGlu 380

Qy  1220 CTTCAGGTGCCCCAGAGCCACTACCTGCTTCCTCTGCAGAAACCGTTTTCATCCATGCCA 1279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 LeuGlnValAlaProLeuProLeuAlaSerSerProGluProPheSerSerMetPro 400

Qy  1280 CCTGCTGCCAGATGTCCTGGTGACACAGGAGGGTGGTCGCCCATTGGGCTTCAGGAGACC 1339
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 ProAlaAlaAspValLeuValThrGlnGluValValProIleGlySerGlnThr 420

Qy  1340 ACACAGTCTGAAACTTCAGGCCCTTCAGCAGCAGCAGGAAACTGGGGGATCCTTGTTTACCT 1399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ThrGlnSerGluThrSerGlyProSerAlaAlaGluThrGlyAlaAspProLeuPheThrPro 440

Qy  1400 AGTTGGTTATAAAGGGCCAAAACCCGGAAAAACCAGCTCAACTCACTGGGAGT 1459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 SerTrpTyrLysGlyGlnSerArgLysThrSerSerThrHisGlySer 460

Qy  1460 GAAGGTCTGGGTCAAATAGGGCCCTCTGGGCCATTGAGGAATTCCAGTGTGCAGTCCGGAA 1519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 GluGlyLeuGlyGlnIleGlyProLeuGlyProLeuGluSerSerValGlnSerAlaGlu 480

Qy  1520 GTGGCAGAAGCCGCACCAATGAGCAGCAGCAGCAGTGAGTGGTAGGGAGTCTAGTTCAACT 1579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ValAlaGluGluAlaAlaThrAsnGluGlnAlaAlaValSerGluSerSerSerThr 500

Qy  1580 GCAGGTACCTCTCAGATTGGATTTGAGGCCCCTTCTTCCCCAGGGGGACCGACCTTG 1639
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 AlaAlaThrSerGlnIleGlyPheGluAlaProSerProGlnGlyGlnProArgAlaAlaLeu 520

Qy  1640 GGGAGTGGGGGGTGGGGTGAATCCTGAGCCAGTCTGCACCAGCTGTCTTCTCCTTCCGGTTTG 1699
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Db   521 GlySerGlyGlyGlyValIleLeuLeuSerGlnLeuLeuAlaThrSerProSerProGlyLeu 540

Qy  1700 AATTCCCTAAATGAA 1714
          |||||||||||||||
Db   541 AsnSerLeuAsnGlu 545
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RESULT 3

US-10-775-627-4

; Sequence 4, Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:

; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-775-627-4

Alignment Scores:

Pred. No.:

Score:	3.45e-210
	2809.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	60.92%
DB:	16

Length:	545
Matches:	545
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-775-627A-3 (1-2590) × US-10-775-627-4 (1-545)

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Qy      1 ATGAGCAACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGATCATGGATAACTTG 139
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetSerThrSerLeuAsnTyrLysSerPheSerLysGluGlnGlnThrMetAspAsnLeu 20

Qy     80 GAAAAGCAACTCATCTCTTCCATCTGCCTAGAGATGTTCACCGAAGCCTGTGTCATTCTC 199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeu 40

Qy    140 CCTTGGCCAGCAACACCTGTGCAGAAAATGTCCCAGTGACACTCTTCAGCGGCCTCTAACCG 259
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ProCysGlnHisAsnLeuCysArgLysCysIleAlaSerAspIlePheGlnAlaSerAsnPro 60

Qy    200 TACTTACCCACCAAGAGGAGCCACCCGTTGGGCCATCAGGGGGCGCCTTCCGTGTCCCTCC 319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TyrLeuProThrArgGlyGlyThrThrValAlaSerGlyGlyArgArgPheArgCysProSer 80

Qy    260 TGCAGACATGAGGTGGTGTTAGACAGACATGGGGGTCTTATGGAGCTGCAGAGGAACCTGCTC 379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsnLeuLeu 100

Qy    320 GTGGAAAACATTATTGATAATCTACAAGCACCAGGAATCCACCCAGCCCAAAAAAATTGGAC 439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 ValGluAsnIleIleAspIleTyrGlnGluSerThrArgProGlyLysLysLeuAsp 120

Qy    380 CAGCCCATGTCTGAGAGCATGAAGAGGAACCATCATCTATTGTCGAAAAATTGGAC 499
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GlnProMetCysGluGluHisGluGluArgIleLeuTyrCysGluLysCysGlu 140

Qy    440 CAGCCCATGTCTGAGAGCATGAAGAGGAACCATCATCTATTGTCGAAACTGTGAA 499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGlnValAlaPro 160

Qy    500 GTGCCCACCTGTTCCTTGTGCAAAGGTTTTGGCGCCCATAAGGACTGCCCAGGTGGCTCCC 559
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LeuThrHisValPheGlnArgGlnLeuSerGluAspGlyIleAlaAlaLeuVal 180

Qy    560 CTGACTCATGTTTTCCAGAGGCAGAAGTCAGTGGTGAATTGCTGTACTTGTG 619
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GlySerAsnAspArgValGlnValIleSerGlnLeuGluLeuAspThrCysLysThrIle 200

Qy    620 GGAAGCAACGATAGAGTCCAGGGTGTGAATCAGCCAGGTGGAGGACAACCTGTAAAACTATT 679
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Db    201 GluGluCysCysArgArgLysGlnLysAspLeuCysGlyLysProHisSerLeuTyrGly 220
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RESULT 4

US-10-104-047-2643

; Sequence 2643, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: H1-A0105
; FILE REFERENCE: US2003023639Zalel full length cDNA
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2643
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-104-047-2643

Alignment Scores:
Pred. No.:   4.21e-175   Length: 548

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Db    301 GluIleGlnGlyTyrGluIleMetSerAsnPheThrValAsnLeuAsnArgGluGluLysIle 320

Qy   1040 ATCCGTGAAATTGACTTTTCTAGAGAAGAGGAAGAAGAAGAAGATGCCAGAGAAAATAGAT 1099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 IleArgGluIleAspPheSerArgGluGluGluGluGluGluAspAlaArgGluAsn 340

Qy   1100 GAAGAAGGAGAAGGAGAAGGAGATGCCAGTGAAGAGAAGAGTAGAAGAAGAGGAGAAGGAGAG 1159
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 GluGluGlyGluGlyGluGlyAspAlaValGluGlyGluAlaGluGlnGluIleIleAla 360
```

AATTCCCTAAATGAA 1714

AsnSerLeuAsnGlu 545

Score: 2359.50   Matches: 465
Percent Similarity: 90.56%   Conservative: 34
Best Local Similarity: 84.39%   Mismatches: 44
Query Match: 51.17%   Indels: 9
DB: 15   Gaps: 3

US-10-775-627A-3 (1-2590) x US-10-104-047-2643 (1-548)

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Qy    80 ATGAGCACTTCTTCTGAATTACAAGTCTTTCTCCAAAGAGCAGACCATGGATAACTTG 139
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ...MetSerIleSerLeuAsnTyrLysSerPheSerLeuGlnGlnThrThrMetAspAsnLeu 20

Qy   140 GAAAAGAAACTGATCTGTCCCACTCGCCTAGAGATGTTCACGAGAGCCGTGCATTCTC 199
Db    21 GluLysGlnLeuIleCysProIleCysLeuGluMetPheThrLysProValValLeu 40

Qy   200 CCTTGCCAGCACAACCCTGGTTGCCAGGAAAATGTGCCAGGAAACCCTTAACCCG 259
Db    41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerArgAspIlePheGlnAlaSerAsnPro 60

Qy   260 TACTTACCCACAAGAGGAGGACCACCGGTGGCCATCAGGGGGGCGCCGCTTCCGCTGTCCCTCC 319
Db    61 TyrLeuProThrArgGlyGlyThrThrMetAlaSerGlyGlyArgPheArgCysProSer 80

Qy   320 TGCAGACANGAGGTGGGTGGTTAGCAGCACATGGGGGCTCTATGGGGACTGCGAGAGGACCTGCTC 379
Db    81 CysArgHisGluValValLeuAspArgHisGlyValThrGlyLeuGlnLeuGlnArgAsnLeuLeu 100

Qy   380 GTGGAAAAACATTATTGGATATCTACACGGGGAATCCACAGGGCCAGAAAAATTGGAC 439
Db   101 ValGluAsnIleIleAspIleTyrLysGlyGlnSerThrArgProGluLysLeuSerAsp 120

Qy   440 CAGCCCATGTGTGAGAGCCATGAGAGGAACGCATCAACATCTATTGTCTTGAACTGTGA 499
Db   121 GlnProMetCysGluSerHisGluGluAsnAlaSerIleTyrCysLeuAsnCysGlu 140

Qy   500 GTCCCACCTGTTCCTTGTCGTCCACAGGTTTTTGGGCCCCATAAGACTGCCCAGGGGGTCTCC 559
Db   141 ValProThrCysSerLeuValHisGlyAlaHisLysAspCysGlnValAlaPro 160

Qy   560 CTGACTCCATGTGTTCCAGAGACGGCAGAAGTCAGAGCTCAGGATGGTATTATTCCTGTACTTGTG 619
Db   161 LeuThrHisValPheGlnArgGlnLysSerGluLeuSerAspGlyIleIleLeuLeuVal 180

Qy   620 GGAGCAACGATAGAGTCCAGGGGTGACTGCAGCCAGCCAGCCACCTGTAAAACTATT 679
Db   181 GlySerAsnAspArgValGlnValIleSerGlnLeuGluAspThrCysLysThrIle 200
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RESULT 5
US-10-104-047-2403
; Sequence 2403, Application US/10104047
; Publication No. US2003023639A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US2003023639A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR APPLICATION DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2403
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2403

Alignment Scores:
Pred. No.:
Score: 5.1e-141   Length: 452
Percent Similarity: 75.14%   Matches: 392
Best Local Similarity: 71.11%   Conservative: 22
Query Match: 41.69%   Mismatches: 33
                                          Indels: 105

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DB:

US-10-775-627A-3 (1-2590) x US-10-104-047-2403 (1-452)

                                    15       Gaps:      4

Qy      1 ATGAGCACTTCTCTGAATTACAAAGTCTTCTTCCAAAGAGCAGCAGACCATGGATAACTTG 139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysGluGlnGlnThrMetAspAsnLeu 20

Qy     80 GAAAAAGCAACTGATCTGTCCCATCTGCCTCAGAGATGTTCACGGAAGCCTGTGGTCAATTCTC 199
Db     21 GluLysGlnLeuLeuIleCysProIleCysLeuGluMetPheThrLysProValValIleLeu 40

Qy    140 CCTTGCCAGACAACACCTGTGCAGGAAAGTGCCAGTGAACATCTTCCAGGCCTTCTAACCCG 259
Db     41 ProCysGlnHisAsnLeuCysArgLysCysAlaSerAspIlePheGlnAlaSerAsnPro 60

Qy    200 TACTTACCCACAAGAGGAGGCACCACCGTGGCATCAGGGGCGCGCTTCGCTGTCCCTCC 319
Db     61 TyrLeuProThrArgGlyGlyThrThrMetAlaSerGlyAlaArgPheArgCysProSer 80

Qy    260 TGCAGACATGAGGTGTGTGTTAGACAGGCAGCATGGGTCTTATGGACTGGAGGAACCTGCTC 379
Db     81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnLeuLeu 100

Qy    320 CAGCCCCATGTGTGTGAAGAGCATAGAAGAGGAAATCCAAACATCTATTCTGTCTGAACTGTGAA 439
Db    101 ValGluAsnIleIleGluTyrLysGlyGluSerThrArgProGlyLysGlnLys 120

Qy    380 GTGGAAAAACATTAATTGAATAATTGTACAAGCGGAAATCCAGGCCCAGAAAAAAATGGAC 499
Db    121 GlnProMetCysGluGlyValHisGluGlyIleAsnIleThrTyrArgCysLeuGlu 140

Qy    440 GTGCCCACCCGTCGTTCCTTGTGTGTGAAGGTTTTTGGCGCCATAGGACTAGGTGGCTCCC 559
Db    141 ValProThrCysSerLeuCysValPheGlyGlyAlaHisSerLysAspCysGlnValAlaPro 160

Qy    500 CTGACTCATGTGTCCAGAGGCAGAAGTCAGAGGGTATTGTGTATTGTACTTGTG 619
Db    161 LeuThrHisValPheGlnArgGlnLysSerGluLeuSerAspGlyIleValTyrCysThrCys 180

Qy    560 GGAAGCAACGATAGAGTCCAGGGTGTGATCACCCAGCTGGACGACACCTGTTAAAACTATT 679
Db    181 GlySerAsnAspArgValGlnGlyValIleSerGlnLeuAspAspThrCysLysThrIle 200

Qy    620 GAGGAGTGCTGCAGAAAGCAGAAACGAAAACAGGAGGGACCTGTGTGAGAAATTTGATCACCTATACGGC 739
Db    201 GluGluCysCysArgLysGlnLysArgGlnGluGlyProValGluLysPheAspHisLeuTyrGly 220

Qy    680 ATCCTGGAGGAGGAGGAGGACTGAAATGACCCAAGCCATCACTCGAACACACAGGAGGAGAAA 799
Db    221 IleLeuGluGluGluGluAspXxxLysAsnAspProSerHisHisArgThrHisArgArg 240

Qy    740 CTGGAACATGTCCGACACTTCTTATCAGGAAGTAGTTATTCCGATCACCTGGAGAACGTATCCAAG 859
Db    241 LeuGluHisValArgAlaLeuLeuIleLeuGlyThrSerAspHisLeuGluLeuAsnValSerLys 260

Qy    800 GCCAAGACCCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGCGTTTCAGATGGAGAAACTA 919
Db    261 LeuValGluSerGlyIleGluGlnPheMetAspProGluMetAlaValPheLeuGluGlnAsn 280

Qy    860 TTGGGTGGAGTCAGGGAATCCAGGTTCATCGGGATGAGCGCAGAAATGGCGCTATTTCTGCAGAAT 979
Db    281 AlaLysThrLeuLeuLysIleSerGluAlaSerLysAlaPheGlnMetGluLysIle 300

Qy    920 GAACAAGGTTATGAGATCATGAGCACTTCACTGTCAATTCTCAATAGAGAGAAAATT 1039
Db    301 GluHisGlyTyrGluAsnMetAsnHisPheThrValAsnLeuAsnArgGluGlyLysIle 320

Qy    980 ATCCCGTCGAAATTGACTTTTCTAGA 1093
Db    321 IleArgGluIleAspPheTyrArgGluAspGluGluGlyGlyGlu 340

Qy   1040 GAAGAGGAAGAGGAAGAGAGATGCAGGAGGAA 1093
Qy   1094 ATAGATGAAGAGGAGGAGGAAGAGGAGGAGAGAG 1144
Db    341 GlyGluGluLysGluGluGlyGluGluGlyGluValGlyGlyValGluGluValGluGluGluGlu 360
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RESULT 6
US-10-473-574-8

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Db    341 GlyGluGluLysGluGluGlyGluGluGlyGluValGlyGlyValGluGluValGluGluGluGlu 360
Db    361 AsnValGlnThrGluPheProGlyGluAspProGluLysGluAlaSerGluLeuSer 380
Qy   1145 AATGTTCAAATAGCATCTTCAGGGGAAGGAGGAGGAGTCTGGGAAAAGCTTGCAGAGCGCCTCT 1204
Db    381 GlnVal------GluGluGlnAlaAlaProGlyAlaLeuProValSerSerProGluPro 398
Qy   1205 CAGCTTCCCGCAGAGCTTCAGGTCGCCCAGCACTACCTGCTTCCTCTCCCAGAACCG 1264
Db    399 ProProAlaLeuProProAlaLeuAlaSerAlaProAlaProValThr------ 411
Qy   1265 TTTTCATCCAATGCCACCTGCTGCAGATGTCCTGGTGACACAGGAGGGGGAGGTGGTGCCCATT 1324
Db    411 ----- 411
Qy   1325 GGCTCTCAGCAGCAGCCACCACAGCTGAAACTTCAGGCCCTTCAGCGCGGGAAAACTGCGGGAT 1384
Db    411 ----- 411
Qy   1385 CCCTTGTTTTACCCTAGTTGGTATAAAGGGCCAAAGCGGGAAAAACCAGCTCCAACCCACCT 1444
Db    411 ----- 411
Qy   1445 TGCACTCATGGGAGTGAAAGGTTCTGGGTCAAAATAGGGCCCTTCTGGGATTCCAGT 1504
Db    411 ----- 411
Qy   1505 GTGCAGTCCGAGAAGTGGCCAGAAGCCCGCAACCAATGAGCAGGAGTGGGTAAG 1564
Db    411 ----- 411
Qy   1565 GAGTCTAGTTCAAACTGCAGCTACCTCTCAGATTGGATTGGAGGGCCCCTTTCTCCCAGGA 1624
Db    412 -----GlnIleIleGlyPheGluGlnAlaProLeuGluGlnGly 422
Qy   1625 CAGTCCTGCAGCCTTGGGGAGTGGGGTGGGGGT-GATCCTGAGCGCCAGCTGTCTTC 1683
Db    423 GlnAlaAlaAlaProAlaSerGlySerGlyAlaAspSerGluProAlaAspArgHisIlePhe 442
Qy   1684 TCCTTCTCCTGGTTTGAATTCCCTAAATGAA 1714
Db    443 SerPheSerTrp-LeuAsnSerLeuAsnGlu 452
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;   PRIOR APPLICATION NUMBER: US 60/290,518
;   PRIOR FILING DATE: 2001-05-10
;   PRIOR APPLICATION NUMBER: US 60/288,609
;   PRIOR FILING DATE: 2001-05-04
;   PRIOR APPLICATION NUMBER: US 60/283,769
;   PRIOR FILING DATE: 2001-04-13
;   PRIOR APPLICATION NUMBER: US 60/281,323
;   PRIOR FILING DATE: 2001-04-03
;   PRIOR APPLICATION NUMBER: US 60/280,508
;   PRIOR FILING DATE: 2001-03-29
;   NUMBER OF SEQ ID NOS: 56
;   SOFTWARE: PERL Program

;   SEQ ID NO 8
;   LENGTH: 452
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 284191CD1

US-10-473-574-8
DB:

Alignment Scores:
Pred. No. :                                   Length:        452
Score:              1922.50                   Matches:       392
Percent Similarity:  75.14%                   Conservative:   22
Best Local Similarity: 71.14%                 Mismatches:     33
Query Match:         41.69%                   Indels:        105
DB:                     16                    Gaps:            4

                5.1e-141
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US-10-775-627A-3 (1-2590) x US-10-473-574-8 (1-452)

Qy   80 ATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCAAAGAGCAGCAGACCCATGGATAACTTG 139
         ||||||||||||||||||||||||||||||||...:|||||||||||||||||||||
Db    1 MetSerAlaSerLeuAsnTyrLysSerPheSerLysValGlnGlnThrMetAspAsnLeu 20
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; Patent No. US20020132753A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PT223
;  CURRENT APPLICATION NUMBER:
;  CURRENT FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: US/09/764,864
;  NUMBER OF SEQ ID NOS: 1792
;  Prior application data removed - consult PALM or file wrapper
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 821
;  LENGTH: 414
;  TYPE: PRT
;  ORGANISM: Homo sapiens
; US-09-764-864-821

Alignment Scores:
Pred. No.:            1.96e-126
Score:               1735.50
Percent Similarity:   73.29%
Percent Identity:     69.20%
Best Local Similarity: 37.64%
Query Match:          9

US-10-775-627A-3 (1-2590) x US-09-764-864-821 (1-414)

Length:         414
Matches:        355
Conservative:    21
Mismatches:      33
Indels:         105
Gaps:             4

DB:
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US-10-775-627A-3 (1-2590) x US-09-764-864-821 (1-414)

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Qy   194 ATTCTCCCTTGCCAGGACAACCTGTCCGCAGGAAAATGTGCCACTGACATCTTCCAGGCCTCT 253
          |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db     1 IleLeuProCysGlnHisAsnLeuCysAlaGlyLysCysAlaSerAspIlePheGlnAlaSer 20

Qy   254 AACCCGTACTTACCCACACAAGAGGAGGAGGAGGGGCCATCAGGGGGGCCGCTTCCGCTGT 313
          |||||||||||||||:::::|||||||||||||||||||||||||||||||||
Db    21 AsnProTyrLeuProThrArgGlyGlyThrThrMetAlaSerGlyGlyArgPheArgCys 40

Qy   314 CCCTCCTGCAGACATGAGGTGGTGTTAGACACAGACTGCAGACGGAAC 373
          |||||||||||||||||||||||||||||||||||||||||
Db    41 ProSerCysArgHisGluValValLeuAspArgHisGlyValTyrGlyLeuGlnArgAsn 60

Qy   374 CTGCTCGGTGGAAAACATTATTGATATCTTACAAGCAGAGAATCCACCAGGCCCAGAAAAAAA 433
          ||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db    61 LeuLeuValGluAsnIleIleAspIleTyrLysGlnSerThrArgProGluLysLys 80

Qy   434 TTGGACCAGCCCATGGTGTGAAGAGAAGAGGAACGCATCAACATCTATTGTCTGAAC 493
          |||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db    81 SerAspGlnProMetCysGluValLysGluGluGlyAsnAlaSerThrSerTyrCysLeuAsn 100

Qy   494 TGTGAAGTGCCCACCCTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAAGGACTGCCAGGTG 553
          ||||||||||||||||:::||||||||||||||||||||||||:::|||||||||
Db   101 CysGluValProThrCysSerLeuCysLysValPheGlyAlaHisLysAspCysGlnVal 120

Qy   554 GCTCCCCTGACTCATGTTGTTCCAGAGGCAGAAGTCAGAGCTGATGTGGTATTGCTGTA 613
          |||||||||||||||||||||||||||||||||||||:::
Db   121 AlaProLeuThrHisValPheGlnArgGlnSerGluLeuSerAspGlyIleAlaAla 140

Qy   614 CTTGTGGGAAGCAAACGATAGAGTCCAGGGGTGTGATCCAGCACCTGGAGGACACCTGTAAA 673
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   141 LeuValGlySerAsnAspArgValGlnGlyValIleLeuSerGlnLeuGluAspThrCysLys 160

Qy   674 ACTATTGAGGAGTGCTCCAGAAAGCAGAAACAGGACCTGTGTGAGAAATTTGATCACTTA 733
          ||||||||||||||||||||||||::::|||||||||||||||||||
Db   161 ThrIleGluGluCysSerArgLysGlnLysGlnAspLeuCysGluLysPheAspHisTyrLeu 180

Qy   734 TACGGGCATCCTGGAGGAGGAAGAGACTGAAAATGACCCAAGCCATCACTCGAACACAGGAG 793
          ||||||||||||||||||||||||||||||||||||:::||||||||||
Db   181 TyrGlyIleLeuGluGluGluArgLysAsnGluMetThrGlnAlaIleThrArgThrGlnGlu 200

Qy   794 GAGAAACTGGAACACATGTCCGAACTCTTATCAGGAGAGTATTCCGATCACCTGGAGAAGGTA 853
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 GluLysLeuGluHisValArgAlaLeuLeuIleLysLysTyrSerAspHisLeuGluAsnVal 220

Qy   854 TCCAAGTTGGTGGAGTCAGGAAATCCAGTTCATGGAGTCAGGGAGTATTTCTG 913
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   221 SerLysLeuValGluSerGlyIleGlnPheMetAspGluProGluMetAlaValPheLeu 240
```

```
Qy   914 CAGAATGCCAAGACCCTGTTGCAAAAAGATCGTGGGAAGGCATCAAAAGGCGTTTCAGATGGAG 973
          |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db   241 GlnAsnAlaLysThrLeuLeuGlnLysAspArgGlyLysAlaSerLysGlyValSerAspGlyVal 260

Qy   974 AAAACTAGAACAAAGGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCAATAGAGAAGAA 1033
          |||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db   261 LysSerLeuGluHisGlyTyrGluAsnMetAsnHisPheThrValAsnLeuAsnArgGluGlu 280

Qy  1034 AAAATTATCCGTGAAATTGACTTTTCTAGA---------GAAGAGGAAGAGGAAGAAGATGCA 1087
          ||||||||||||||||||||||||||||||        :::||||||||||||||
Db   281 LysIleIleArgGluIleAspPheTyrArgGluAspGluGluGluGluGluGluGlu 300

Qy  1088 GGAGAAATAGATGAAGAAGAGGAAGAAGAGGAG------------GATGCAGTAGAAGTAGAAGAG 1138
          ||||||||||||||||||||:::                   ||||||||||||||||
Db   301 GlyGluIleAspGluGluGluGluGluGlu-----------AspAlaValGluValGluGlu 320

Qy  1139 GCAGAAAAATGTTCAAAATAGCAATCTTCAGGGGGAAGAGGAGAGTCGTGGAGAAGAGCTGCAGAG 1198
          ||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db   321 ValGluAsnValGlnThrGluPheProGlyValAspGluAsnProLysSerAlaSerGlu 340

Qy  1199 CCCTCTCAGCCTTCCCGCAGAGACTTCAGGTCGCCCCAGAGCCACTACCTGTCTTCCTCTCCA 1258
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 LeuSerGlnVal----------GluLeuGlnAlaAlaProGlyAlaLeuProValSerSerPro 358

Qy  1259 GAAACCGTTTCATCCAATGCCACCTGCTGCAGATGTCCTGGTCACACAGGGGTGGTG 1318
          |||||||||||||||||||||||||||||||||||||||||||
Db   359 GluProProProAlaLeuProProProAlaLeuAlaAspAlaProValThr------ 373

Qy  1319 CCCATTGGCTCTGCAGAGACCACACAGTCTGAAACTTCAGCGCAGCGGAAACT 1378
          |||||||||||||||||||||||||||||||||:::
Db   373 -------------------------------------- 373

Qy  1379 GCGGATCCCTTGTTTTTTACCCTAGTTGGTGTATAAAAGGCCAAAGCCGGAAAAACCAGCTCCAAC 1438
          |||||||||||||||||||||
Db   373 -------------------------------------- 373

Qy  1439 CCACCTTGCACTCATGGGAGTGAAAGGTTCTGGGTCAAATAGGGGCCCTCTGGGCATTGAGGAT 1498
          ||||||||||||||||
Db   373 -------------------------------------- 373

Qy  1499 TCCAGTGTGCAGTCCCCGAGAAGTGGCCAGAAGCCCGCAACCAAATGAGCAGGCAGCAGTGAGT 1558
          ||||||||||||
Db   373 -------------------------------------- 373

Qy  1559 GGTAAGGAGTCTTAGTTCAAACTGCCAGTTCACCTCTTCAGATTGGAATTTGAGGCCCCTTCTCCC 1618
          |||||
Db   374 ------------------GlnIleGlyIlePheGluValAlaProProLeu 382

Qy  1619 CAGGGACAGTCTGCCAGCCTTGGGAGTGGGGGTGGGGT-GATCCTGAGCCAGCTGCCGCCAC 1677
          |||||||||||||||||||||||||||||||
Db   383 GlnGlyValAlaAlaAlaAlaProAlaSerGlySerGlyValAlaAspSerGluProAlaArgHis 402

Qy  1678 GTCTTCTCCTCTCTCCTGGTTTGAATTCCCTAAAATGAA 1714
          :::||||||||||||||||
Db   403 IlePheSerPheSerTrp-LeuAsnSerLeuAsnGlu 414
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RESULT 8
US-09-890-688-58
; Sequence 58, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
;  APPLICANT: Seishi KATO
;  APPLICANT: Chikashi EGUCHI
;  APPLICANT: Mihoro SAEKI
;  TITLE OF INVENTION: Human Proteins and cDNAs thereof
;  FILE REFERENCE: 2001-1102A/WMC/00653
;  CURRENT APPLICATION NUMBER: US/09/890,688
;  CURRENT FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: JP 11-346863
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: JP 11-34684
;  PRIOR FILING DATE: 1999-12-06
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; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-34090
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-35829
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 58
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-890-688-58

Query Match: 25.29%

Alignment Scores:
Pred. No.:
Score: 5.29e-82
Score: 1166.00

Best Local Similarity: 64.59%
Percent Similarity: 77.62%

	Length:	358
	Matches:	228
	Conservative:	46
	Mismatches:	73
	Indels:	6
	Gaps:	3

US-10-775-627A-3 (1-2590) x US-09-890-688-58 (1-358)

Qy   80 ATGAGCACTTCTCTGAATTACAAGGTCTTTCTCCAAAGAGACGAGCAGACCATGGATAACTTG 139
        |||.|::| ::||.| ||.||
Db   1 MetAsnPheThrValGlyPheLysProLeuLeuGlyAspAlaHisSerMetAspAsnLeu 20

Qy 140 GAAAAGCAACTGATCTCTGTCTCCCATCTGCCTAGAGATGTTCACGAAGGCCTGTGGTCATTCTC 199
        |||||| :::||:||:||:
Db   21 GlyLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValLeu 40

Qy 200 CCTTGCCAGCACAACCTGTCGCAGGAAATGTGCCAGTGACATCTTCCAGGCCTCTAACCCG 259
        |||||||||||||||||||||||||
Db   41 ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro 60

Qy 260 TACTTTACCCACAAGAAGGAGGAGCACCGTGGCATCGGGGGCCGCTTCCGCTGTCCCCTCC 319
        ::||:||||||
Db   61 LeuTrpSerArgGlySerThrThrValSerSerGlyIleArggPheArgCysProSer 80

Qy 320 TGCAGACATGAGAGTGGTGTTAGACAGACATGGGGTCGTCTATAGGGAACCTGCTCTC 379
        |||||||||||||||||
Db   81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLysGlnArgAsnLeuLeu 100

Qy 380 GTGGGAAAACATTATTGATATACTACAAGACAGGAATCCACAGGCCA---GAAAAAAATTG 436
        ||||||| |:::|| ::||:||:||
Db 101 ValGluAsnIleIleAspIleTyrGlnThrGlnGlySerLysAlaGln 120

Qy 437 GACCAGCCC---ATGTGTGAAGAGACGGACGCATCAACACATCTATTGTCTGAAC 493
        ::||||||||||||||||||||||||||||||
Db 121 GluGlnHisLeuMetCysGluGluHisGluGlyLysIleAsnIleTyrCysLeuSer 140

Qy 494 TGTGAAGTGCCCACCTGTTCCTTGTGCAAGGGTTTTGGGGCGCCCCATAAGGACTGCCAGGTG 553
        |||||||||||||||||||||||||||||
Db 141 CysGluLysValProThrCysSerLeuCysLysGlyValPheGlyAlaHisLysAspCysGluVal 160

Qy 554 GCTCCCCTGACTCATGTTGTTCCAGAGGCACAGAAGTCAGAGTCGATGGTATTGCTGTA 613
        |||||| | :::||:||:::||:
Db 161 AlaProLeuProThrIleTyrLysArgArgGlnLysSerGluSerAspGlyIleLeuAlaMet 180

Qy 614 CTTGTGGGAAGCAACGATAGAGTCCAGGGTGTTGATGATGGACACCTGTAA 673
        |||||||||||||||||||||
Db 181 LeuValAlaGlyAsnAspArgValGlnAlaValIleThrArgGlnMetGluValValCysGln 200

Qy 674 ACTATTGAGGAGTGCTGCAGAAAAGAGAGAAACAGGACCTGTGTGTGGAAATTTGATCACCTA 733

Db 201 ThrIleGluAspAsnSerArgArgGlnLysGlnLeuLeuAsnGlnArgPheGluSerLeu 220

RESULT 9
US-09-908-988B-2
; Sequence 2, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-908-988B-2

Query Match: 25.20%

Alignment Scores:
Pred. No.:
Score: 1.09e-81
Score: 1162.00

Best Local Similarity: 61.92%
Percent Similarity: 76.99%

	Length:	366
	Matches:	226
	Conservative:	55
	Mismatches:	76
	Indels:	8
	Gaps:	4

US-10-775-627A-3 (1-2590) x US-09-908-988B-2 (1-366)

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Qy 140 GAAAAGCAACTGATCTCTGTCTCCCATCTGCCTAGAGATGTTCACGAAGGCCTGTGGTCATTCTC 199
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Db   21 GlyLysGlnLeuIleCysProIleCysLeuGluMetPheSerLysProValValLeu 40

Qy 200 CCTTGCCAGCACAACCTGTCGCAGGAAATGTGCCAGTGACATCTTCCAGGCCTCTAACCCG 259
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Db   41 ProCysGlnHisAsnLeuCysArgLysCysAlaAsnAspValPheGlnAlaSerAsnPro 60

Qy 260 TACTTTACCCACAAGAAGGAGGAGCACCGTGGCATCGGGGGCCGCTTCCGCTGTCCCCTCC 319
        ::||:||||||||:::||||||:::
Db   61 LeuTrpSerArgGlySerThrThrValSerSerGlyIleArggPheArgCysProSer 80

Qy 320 TGCAGACATGAGAGTGGTGTTAGACAGACATGGGGTCGTCTATAGGGAACCTGCTCTC 379
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Db   81 CysArgHisGluValValLeuAspArgHisGlyValTyrGlyLysGlnArgAsnLeuLeu 100

Qy 380 GTGGGAAAACATTATTGATATACTACAAGACAGGAATCCACAGGCCA---GAAAAAAATTG 436
        ||||||| |:::|| ::||:||:||:::
Db 101 ValGluAsnIleIleAspIleTyrGlnThrGlnGlySerLysAlaGln 120

Qy 437 GACCAGCCC---ATGTGTGAAGAGACGGACGCATCAACACATCTATTGTCTGAAC 493
        ::||||||||||||||||||||||||||||||:::
Db 121 GluGlnHisLeuMetCysGluGluHisGluGlyLysIleAsnIleTyrCysLeuSer 140

Qy 494 TGTGAAGTGCCCACCTGTTCCTTGTGCAAGGGTTTTGGGGCGCCCCATAAGGACTGCCAGGTG 553
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Db 141 CysGluLysValProThrCysSerLeuCysLysGlyValPheGlyAlaHisLysAspCysGluVal 160

Qy 554 GCTCCCCTGACTCATGTTGTTCCAGAGGCACAGAAGTCAGAGTCGATGGTATTGCTGTA 613
        |||||| | :::||:||:::||:
Db 161 AlaProLeuProThrIleTyrLysArgArgGlnLysSerGluSerAspGlyIleLeuAlaMet 180

Qy 614 CTTGTGGGAAGCAACGATAGAGTCCAGGGTGTTGATGATGGACACCTGTAA 673
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Db 181 LeuValAlaGlyAsnAspArgValGlnAlaValIleThrArgGlnMetGluValValCysGln 200

Qy 674 ACTATTGAGGAGTGCTGCAGAAAAGAGAGAAACAGGACCTGTGTGTGGAAATTTGATCACCTA 733

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Qy 734 TACGGCCATCCTGGAGGAGGAGGAGAAGACTGAAATGACCCAGCACTCACTGGAACACAGGAG 793
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Db 241 GluLysLeuGlnArgValArgGlyLeuLeuLeuArgGlnThrGlyAspPheLeuGluAlaSer 260

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Qy 914 CAGATAGTGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAAGGCGTTTCAGATGAG 973
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; APPLICANT: SPENCER, JEFFREY A.
; APPLICANT: OLSON, ERIC
; GENERAL INFORMATION:
; Publication No. US20040132160A1
; Sequence 2, Application US/10775649
US-10-775-649-2
RESULT 10

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD2
; CURRENT APPLICATION NUMBER: US/10/775,649
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-775-649-2

Alignment Scores:
Pred. No.:
Score: 1162.00
Percent Similarity: 76.99%
Best Local Similarity: 61.92%
Query Match: 25.20%
DB:

Length: 366
Matches: 226
Conservative: 55
Mismatches: 76
Indels: 8
Gaps: 4

US-10-775-627A-3 (1-2590) x US-10-775-649-2 (1-366)

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Qy    261 SerLysLeuValGluSerAlaIleGlnSerMetGluGlnProGlnMetAlaLeuTyrLeu 280
Db    914 CAGGAATGCCAAGACCCTGTTGCAAAAGATCCGTGGAAGCATAAAGGCGTTTCAGATGGAG 973
Qy    281 GlnGlnAlaLysGluLeuIleAsnLysValGlyAlaMetSerLysProValValIleLeu 300
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Qy    301 ArgProGlyTyrGluSerMetGluGlnPheSerValSerGluHisValAla 320
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Qy    361 GluGlySerGlyLeu 365

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; Sequence 2, Application US/10775627
; Publication No. US20040124446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-775-627-2

Alignment Scores:
Pred. No.:              1.09e-81
Score:                  1162.00       Length:         366
Percent Similarity:     76.99%        Matches:        226
Best Local Similarity:  61.92%        Conservative:   55
Query Match:            25.20%        Mismatches:     76
DB:                     16            Indels:         8
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US-10-775-627A-3 (1-2590) x US-10-775-627-2 (1-366)

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Qy    221 CysAlaValLeuGluLeuGluArgLysGlyGluLeuLeuGlnAlaLeuAlaArgGluGlnGlu 240
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Qy    241 GluLysLeuGlnArgValArgGlyLeuIleLeuArgGlnTyrGlyAspHisLeuGluGlySer 260
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Qy    301 ArgProGlyTyrGluSerMetGluGlnPheSerValSerGluHisValAla 320
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Qy    341 MetAlaLeuAspGlyGluGlyGlyAsnAlaGlyLeuGluGluArgLeuAspValPro 360
Db   1136 GAGGCAGAAAATGTT 1150
Qy    361 GluGlySerGlyLeu 365

RESULT 12
US-10-204-921-57
; Sequence 57, Application US/10204921
; Publication No. US20050095587A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
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; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: JACKSON, Stuart

; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1133 PCT
; CURRENT APPLICATION NUMBER: US/10/204,921
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/185,213; 60/205,285; 60/205,232; 60/205,323; 60/205,287;
  60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-05-17; 2000-05-16; 2000-05-17; 2000-05-17;
  2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PERL Program

; SEQ ID NO 57
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:247384.1.orf2:2000MAY19

US-10-204-921-57

US-10-775-627A-3 (1-2590) x US-10-204-921-57 (1-366)

Alignment Scores:

Pred. No.:                                      Length:         366
Score:              6.24e-80                    Matches:        226
Percent Similarity: 1139.50                     Conservative:   51
Best Local Similarity: 73.47%                   Mismatches:     77
Query Match:        59.95%                       Indels:         23
DB:                 24.71%                       Gaps:           3
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Db    71 TyrLeuProThrArgGlyGlyTyrThrMetAlaSerGlyTyrArgPheArgCysProSer 90
Qy   320 TGCAGACATGAGGTGGTGTTAGACAGACATGGGGTGGGTCTTATGGACTGCCGAGAGAACCTGCTC 379
Db    91 CysArgHisGluValValLeuAspArgHisGlyIleValTyrGlyLeuGlnAsnLeuLeu 110
Qy   380 GTGGGAAAACATTATTCATTACATACAAGCAGAA---TCCACCAGGCGCCAGAAAAAATTG 436
Db   111 ValGluAsnIleIleAspIleTyrLysSerSerArgProLeuGlnLysGly 130
Qy   437 GACCAGCCCATGTGAAGAGGCATGAAGAGAAGACCATCAACACATCTATTGTCTGAACTGT 496
Db   131 SerHisProMetCysLysGluHisGlyLysArgYCysLeuThrCys 150
Qy   497 GAAGTGCCCACCTGTTCCTTGTCCAAGGTTTTGGGGCCCCATAAGGACTGCCAGGTGGCT 556
Db   151 GluValProThrCysSerMetCysLysValPheGlyLysGluValAla 170
Qy   557 CCCCTGACTCAGTGTTCCAGAGGGCAGAAGTCAGAGGCTCAGTGATGTAGTTGCTGTACTT 616
Db   171 ProLeuGlnSerValPheGluGlyGlnLysThrGlyLeuGlnLeuAsnAsnCysIleSerMetLeu 190
Qy   617 GTGGGAAGCCAACGATAGAGTCCAGGGTGTGGATCAGGAGAAGTATTCAGCGGAACGTATCC 676
Db   191 ValAlaGlyAsnAspArgValGlnThrIleLeuThrGlnLeuAsnGluAsnSerArgArgVal 210
Qy   677 ATTGAGGAGTGGTGCTGCAGAAACCAGACAGAACCTGTTGTGAGAAATTGATCACTTATAC 736
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Qy   737 GGCATCCTTGGCGGAGGAGGAGAGAGACTGAAATGACCCAGCCATCACTGATTGTGACGAGG 796
Db   231 AlaIleLeuAspGlyLysSerLysSerGluGlnGlnArgIleThrGlnLeuGlnGlyLys 250
Qy   797 AAAACTTGGAACACATGTCCGAACTCTTATCAGCGAAGTATTCCGATCACCTGGAGAGTATCC 856
Db   251 LysLeuSerPheIleGluValAlaLeuIleLeuGlnIleThrGlnLeuLeuAspSerThr 270
Qy   857 AAGTTGGTTGGAGTCAGGAATCCAGTTCATGGAGCAACTTCACTGTCAAATCTCAATAGAGAA 916
Db   271 LysLeuValGluThrGlyIlePheGluAsnMetAspPhePheThrLeuAspAspThrLeuLeu 290
Qy   917 AATGCCAAGACCCTGTTGCAAAAGATCGTTGGAAGCATCAAAGGCGTTTCAGATGGAGAA 976
Db   291 ThrAlaLysThrLeuLeuLysSerIleValGlyAlaIleSerIleGlyValLys 310
Qy   977 CTAGAACAAGGTTATGAGATCATGGAGCAACTTCACTGTGAAATCTCAATAGAGAAGAAGAAA 1036
Db   311 ThrGluGlnGlyTyrPheGluAsnMetAspPhePheThrLeuAspLeuHisIleAlaAsp 330
Qy  1037 ATTATCCGTGAAATTGACTTTTCTAGAGAAGAGGAGAAGGAGGAGGATGCAGGAGAATA 1096
Db   331 AlaLeuArgAlaIleAlaAspPheGlyTyrAspAspPheGlyIleGluGlu 350
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RESULT 13
US-10-061-043A-37
; Sequence 37, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
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Qy   200 CCTTGCCAGCACAACCTTGTCGAGGAAAATGTCCCAGTGACACTCTTCCAGGCCTTCTCAAACCCG 259
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Qy   140 GAAAAGCAAACTCATCTCTCCCATCTGCCTAGAGATGTTCACGAAAGCCTGTGTGGTCATTCTC 199
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Qy    11 SerHisArgMetAspTyrLeuSerSerLeuIleLeuAspGlyAsnProMetGluAsnLeu 30
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:        June 14, 2005, 16:12:56 ; Search time 1270 Seconds
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Perfect score: 2590
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:  8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	Match ID	Description
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23	436	16.8	1781	8	ABX73183	Abx73183 Human nov
24	432.2	16.7	1597	6	ABA99063	Aba99063 Murine mu
25	419.4	16.2	867	6	ABQ79512	Abq79512 Human MUR
26	376.6	14.5	573	10	ADC32553	Adc32553 Human nov
27	373.6	14.4	587	4	AAS26314	Aas26314 Human CDN
28	373.6	14.4	587	8	ABX73655	Abx73655 Human nov
29	361.4	14.0	1183	5	AAH90117	Aah90117 Human bon
30	344.8	14.0	1796	5	AAH89924	Aah89924 Human bon
31	344.4	13.3	1500	4	AAF27653	Aaf27653 DNA encod
32	308.6	11.9	2040	6	ABN85313	Abn85313 Human cyt
33	288.2	11.1	498	8	ABQ79510	Abq79510 Rat MURF1
34	285.2	11.0	498	9	ACH44808	Ach44808 Human foe
35	284	11.0	391	3	AAC75969	Aac75969 Human ORF
36	243.8	9.4	496	9	ACH15746	Ach15746 Human adu
37	241.8	9.3	531	3	AAC75285	Aac75285 Human ORF
38	241.8	9.3	531	3	ABN78104	Abn78104 Human int
39	206.6	8.0	2762	12	ADP22641	Adp22641 Sea-squir
40	167	6.4	424	9	ACH18104	Ach18104 Human adu
41	156.6	6.0	411	9	ACH17597	Ach17597 Human adu
42	151	5.8	446	4	AAS26303	Aas26303 Human CDN
43	151	5.8	446	8	ABX73644	Abx73644 Human nov
44	140.4	5.4	1039	6	AAD42866	Aad42866 Human DNA
45	140.4	5.4	1039	10	ADH62597	Adh62597 Human ven

```
                              ALIGNMENTS

RESULT 1
ABA99062

ID   ABA99062 standard; DNA; 2590 BP.
XX
AC   ABA99062;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Murine muscle ring finger protein 2 (MURF-2) coding sequence.
XX
KW   Muscle ring finger; MURF-2; mouse; cardiant; microtubule;
KW   intermediate filament; striated muscle; cardiac hypertrophy;
KW   heart disease; gene; ds.
XX
OS   Mus musculus.
XX
FH
FT   Key             Location/Qualifiers
FT   CDS             80..1717
FT                   /tag= a
FT                   /product= "MURF-2"
XX
PN   WO200206318-A2.
XX
PD   24-JAN-2002.
XX
PF   18-JUL-2001; 2001WO-US022896.
XX
PR   18-JUL-2000; 2000US-0219020P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Olson EN,   Spencer JA;
XX
DR   WPI; 2002-241506/29.
DR   P-PSDB; ABB08276.
XX
PT   Novel muscle ring finger protein useful for drug screening, and for
PT   diagnosing and treating diseases, particularly cardiomyopathies.
PS   Claim 4; Page 126-129; 134pp; English.
XX
CC   The sequence encodes murine muscle ring finger protein 2 (MURF-2).
CC   invention relates to a purified muscle ring finger (MURF) protein,
```

CC   selected from MURF-1, MURF-2 and MURF-3. The MURF proteins of the
CC   invention are involved in microtubule and intermediate filament
CC   stabilisation of striated muscle cells and have cardiant activity. The
CC   MURF proteins are useful for screening a candidate substance for MURF
CC   protein-binding activity, in a cell, cell-free system or in vivo, and its
CC   effect on interaction of MURF with microtubules, homodimerisation of
CC   MURF, MURF-1, MURF-2 or MURF-3 stabilisation of microtubules, interaction
CC   of MURF with intermediate filaments, e.g. desmin, vimentin and
CC   cytokeratin, and heterodimerisation of MURF. The screened compounds are
CC   useful for treating and preventing cardiac hypertrophy and heart
CC   diseases. MURF proteins are useful as antigens to immunise animals for
CC   the production of antibodies
XX
SQ   Sequence 2590 BP; 703 A; 627 C; 625 G; 635 T; 0 U; 0 Other;

Query Match   100.0%; Score 2590; DB 6; Length 2590;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CTCGAGATTTACCCTTACAGAGAAGCTGTTTCGGGAGCACCACTTTCCCTTGGCAGCACTCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTCGAGATTTACCCTTACAGAGAAGCTGTTTCGGGAGCACCACTTTCCCTTGGCAGCACTCAG 60

Qy   61 GGACAGGGACGGCAAGGAAATGAGACACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGACAGGGACGGCAAGGAAATGAGACACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120

Qy   121 GCAGACCATGGATAACTTGGAAAAAGCAAACTTGGAAAAAGCAAACTGCCTAGAGATGTTCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCAGACCATGGATAACTTGGAAAAAGCAAACTTGGAAAAAGCAAACTGCCTAGAGATGTTCAC 180

Qy   181 GAAGCCCTGTGGGTCATTCTCCCTTGCCAGCACAACCTTGTCCAGGAAAATGTGCCAGTGACAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTTCCAGGCCCTGTTCATTCTCCCTGCCAGCACAACCTTGTCCAGGAAAATGTGCCAGTGACAT 240

Qy   241 CTTCCAGGCCCTGTTCATTCTCCCTGCCAGCACAACCTTACCCACACAGAGGAGGGTCTCTATGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCGCTTCCGCTGTCCCTCTCGTCGGTGAAAAACATTATTGATATCTACAAGCAGCAGAATCCACCAG 300

Qy   301 CCGCTTCCGCTGTCCCTCTCGTCGGTGAAAAACATTATTGATATCTACAAGCAGCAGAATCCACCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACTGCAGAGGAACCTGCTCGTCGGTGAAAAACATTATTGATATCTACAAGCAGCAGAATCCACCAG 360

Qy   361 ACTGCAGAGGAACCTGCTCGTCGGTGAAAAACATTATTGATATCTACAAGCAGCAGAATCCACCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCCAGAAAAAAATTGGACACCAGCCCATGTGTGAAGAGCCATGAAGAACCCATCAACAT 420

Qy   421 GCCAGAAAAAAATTGGACACCAGCCCATGTGTGAAGAGCCATGAAGAACCCATCAACAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGTCCAAGGTTTTTTGGGGCCCATAA 480

Qy   481 CTATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGTCCAAGGTTTTTTGGGGCCCATAA 540
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Db   481 GGACTGCCAGGTGGCTCCCTGACTCATGTGTTGTTCCAGAGGACCTCAGTGA 540

Qy   541 GGACTGCCAGGTGGCTCCCTGACTCATGTGTTGTTCCAGAGGACCTCAGTGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGGTATTGCTGTACTTGTGGGAAGCAACGATTAGAGTCCAGGGTGTCAGCCAGCTGGA 600

Qy   601 TGGTATTGCTGTACTTGTGGGAAGCAACGATTAGAGTCCAGGGTGTCAGCCAGCTGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGACACCGTGTAAAACTATTGAGGAGTGCTGCAGAAAGACAGACAGCTGTGTGTGAGAA 660

Qy   661 GGACACCGTGTAAAACTATTGAGGAGTGCTGCAGAAAGACAGACAGCTGTGTGTGAGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AATTTGATCACCTTATACGGCATCCTGGACGAGGAGGAAGAGACTGAAAATGACCCAAGCACTCT 720

Qy   721 AATTTGATCACCTTATACGGCATCCTGGACGAGGAGGAAGAGACTGAAAATGACCCAAGCACTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCGAACACAGGAGGAGAAACTGGAACATGTCCGGAACTCTTATCAGGAAGAAGTATTCCGATCA 780

Qy   781 TCGAACACAGGAGGAGAAACTGGAACATGTCCGGAACTCTTATCAGGAAGAAGTATTCCGATCA 840
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Db   781 CCTGGAGAAACGTATCCAAGTTGGTTGGTGGAGTCAAGTTCAGTGGGATGAGCCCCGAAAT 840

Qy   841 CCTGGAGAAACGTATCCAAGTTGGTTGGTGGAGTCAAGTTCAGTGGGATGAGCCCCGAAAT 900
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Db   841 GGCAGCGTATTTCTGCAGAATGCCAAGACCCTTGCAAAGAATCAAAGGC 900

Qy   901 GGCAGCGTATTTCTGCAGAATGCCAAGACCCTTGCAAAGAATCAAAGGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCT 960

Qy   961 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCT 1020
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Db   961 CAATAGGAGAGGAAGAGAAAATTATCCGTGAAAATTGACTTTTCTAGAGAAGAGGAAGAGGAGGAAGA 1020

Qy   1021 CAATAGGAGAGGAAGAGAAAATTATCCGTGAAAATTGACTTTTCTAGAGAAGAGGAAGAGGAGGAAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGATGCAGGAGAGAAATAGGATAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGC 1080

Qy   1081 AGATGCAGGAGAGAAATAGGATAGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGC 1140
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Db   1081 AGAAAAAATGTTCAAAATAGCATCTTCAGGGAAGAAGGAGTCTGGAGAAGTTGCAGAGCC 1140

Qy   1141 AGAAAAAATGTTCAAAATAGCATCTTCAGGGAAGAAGGAGTCTGGAGAAGTTGCAGAGCC 1200
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Db   1141 CTCTCAGCTTCCCGCGAGAGCTTCAGGTCGCGCCCCAGAGCCCACTACCTGCTTCCTCCAGA 1200

Qy   1201 CTCTCAGCTTCCCGCGAGAGCTTCAGGTCGCGCCCCAGAGCCCACTACCTGCTTCCTCCAGA 1260
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Db   1201 ACCGTTTTCATCCATGGCCACCGCCACTGCTGCCAGAGTGTCCTGGTGGTGCACACAGGGGTGGTGCC 1260

Qy   1261 ACCGTTTTCATCCATGGCCACCGCCACTGCTGCCAGAGTGTCCTGGTGGTGCACACAGGGGTGGTGCC 1320
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Db   1261 CATTGGCTCTCAGCGACACAGACCACAGTCAGAGTTGAAACTTCAGCGGCGGGGAAAACCC 1320

Qy   1321 CATTGGCTCTCAGCGACACAGACCACAGTCAGAGTTGAAACTTCAGCGGCGGGGAAAACCC 1380
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Db   1321 GGATCCCTTGTTTTACCCTAGTTGGTTGTTATAAAGGCCAAAGACCAGCAGTGAGTGG 1380

Qy   1381 GGATCCCTTGTTTTACCCTAGTTGGTTGTTATAAAGGCCAAAGACCAGCAGTGAGTGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACCTTGCACTCAATGGGAGTGAAAGGTCTGGGTCAAATAGGGCCTTCTCTGGGCATTGAGGAATTC 1440

Qy   1441 ACCTTGCACTCAATGGGAGTGAAAGGTCTGGGTCAAATAGGGCCTTCTCTGGGCATTGAGGAATTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CAGTGTGCCAGTCCGCAGAAGTGCAGAGCGCAACCAATGAGCAGGCCAGTGAGTGG 1500

Qy   1501 CAGTGTGCCAGTCCGCAGAAGTGCAGAGCGCAACCAATGAGCAGGCCAGTGAGTGG 1560
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Db   1501 GGATCCCTTTGTTCAACTGCAGAGCTACCTCTCAGATTGGATGGAGGCCCCCTTCTCCCCA 1560

Qy   1561 GGATCCCTTTGTTCAACTGCAGAGCTACCTCTCAGATTGGATGGAGGCCCCCTTCTCCCCA 1620
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Db   1561 TAAGGAGTCTAGTTCAACTGCAGCTACCTCTCAGATTGGAGGCCCCCTTGAGCTGCCACGTC 1620

Qy   1621 GGGACAGTCTGCAGCCCTTGGGAGTGGGGGTGGGTTGATCCTGACGCTGCAGCCCACGTC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GGGACAGTCTGCAGCCCTTGGGAGTGGGGGTGGGTTGATCCTGACGCTGCAGCCCACGTC 1680

Qy   1681 TTCTCCTTCTCCTGGGTTTGAATTCCCTAAAATGAATAATATTTTATTTCTGTTGCCCCC 1740
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Db   1681 TTCTCCTTCTCCTGGGTTTGAATTCCCTAAAATGAATAATATTTTATTTCTGTTGCCCCC 1740

Qy   1741 TGTCTGCCTGGCTGAAAAGCACATAGGCAGCAGAAACAGGTGGAAATTCACCACGATTC 1800
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Db   1741 TGTCTGCCTGGCTGAAAAGCACATAGGCAGCAGAAACAGGTGGAAATTCACCACGATTC 1800

Qy   1801 ATATGAAGGGGACACCTTGGACAGGATTTCTGAAAGACAAAAACAAATACAACAACCACC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATATGAAGGGGACACCTTGGACAGGATTTCTGAAAGACAAAAACAAATACAACAACCACC 1860

Qy   1861 ACCCTTTAATTCCAGATGACTTATCTCCACTCATTGAGAAAATGATTATGTGCTCAGAACAAA 1920
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Db   1861 ACCCTTTAATTCCAGATGACTTATCTCCACTCATTGAGAAAATGATTATGTGCTCAGAACAAA 1920

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RESULT 2
ADB62519
ID   ADB62519 standard; cDNA; 1925 BP.
XX
AC   ADB62519;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human cDNA encoding clone HEART20019310.
XX
KW   Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW   tissue regeneration; cell regeneration; membrane protein;
KW   signal transduction-related protein; transcription-related protein;
KW   osteoporosis; neurological disease; cancer; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             47..1693
FT                   /tag= a
FT                   /product= "Clone HEART20019310 protein"
XX
PN   EP1308459-A2.
```

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Qy  1921 ATTACAGAAAATACTCTTCTTCGAAGAAACTTGATCTTCATTTGTGTGAG 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 ATTACAGAAAATACTCTTCTTCGAAGAAACTTGATCTTCATTTGTGTGAG 1980

Qy  1981 AAACCTTCTGAAGGTTGTGTGTAGGTGTTGGTGGCCATAAGTGCCAAG 2040
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AAACCTTCTGAAGGTTGTGTGTAGGTGTGGTGGCCATAAGTGCCAAG 2040

Qy  2041 TGGTAACAAAGTGGCAGAACACTCTCCAGCCTTCTCCTCCAGGCTTCTTCGGTTGTTATTTAGGAC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2040 TGGTAACAAAGTGGCAGAACACTCTCCAGCCTTCTCCTCCAGGCTTCTTCGGTTGTTATTTAGGAC 2100

Qy  2101 GCTTGTGCCTTTTGCCTTTGCTTTGTTCCCTTAGCATTGCAGGTGGTAGGTGATTGTTCAGTGTCAGT 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 GCTTGTGCCTTTTGCCTTTGCTTTGTTCCCTTAGCATTGCAGGTGGTAGGTGATTGTTCAGTGTCAGT 2160

Qy  2161 TCCAAACTGACCGATTTATCAAAAATATGGAGATTGGTCACTGACCAAAGCTATGTGTAGGGC 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 TCCAAACTGACCGATTTATCAAAAATATGGAGATTGGTCACTGACCAAAGCTATGTGTAGGGC 2220

Qy  2221 ACTGTAGAGGTTCCTTTCCCTATGGATGCCATGGGTGCGCGAGACAGGACTTTCCTTTACA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 ACTGTAGAGGTTCCTTTCCCTATGGATGCCATGGGTGCGCGAGACAGGACTTTCCTTTACA 2280

Qy  2281 TGTGGCCACACGTCCATAGTCCAGAAGGCCAAAAAATCTAGGGCAACTCTTTGACATTTT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TGTGGCCACACGTCCATAGTCCAGAAGGCCAAAAAATCTAGGGCAACTCTTTGACATTTT 2340

Qy  2341 TCTAACCTTATTTACATATCTCATTAATCATATAAGTATTAGGGCATTTTAATTGAATTT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TCTAACCTTATTTACATATCTCATTAATCATATAAGTATTAGGGCATTTTAATTGAATTT 2400

Qy  2401 CAAAGAGGAGCTGTCTACTTTCTTAAGTGTCTGCCATAGCCAGCCAAATCTGATATAATCTGTG 2460
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Db  2401 CAAAGAGGAGCTGTCTACTTTCTTAAGTGTCTGCCATAGCCAGCCAAATCTGATATAATCTGTG 2460

Qy  2461 GAGCAACTGCATGGATTTAAGTATACACACAAATTCTCCCCCCTGTGTGTGGCCTTCTCTCTCTC 2520
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Db  2461 GAGCAACTGCATGGATTTAAGTATACACACAAATTCTCCCCCCTGTGTGTGGCCTTCTCTCTCTC 2520

Qy  2521 TCTCTCTCCCCCCTGTCTCTCTCCCCTGTCTCTCTCTCCTTCTCTCTCTCTCCT 2580
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Db  2521 TCTCTCTCCCCCTGTCTCTCTCCCCTGTCTCTCTCTGCGCTTCTCTCCTTCTCTCTCTCTCCT 2580

Qy  2581 TTCTCCTCC 2590
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Db  2581 TTCTCCTCC 2590
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XX
PD   07-MAY-2003.
XX
     28-MAR-2002; 2002EP-00007401.
XX
PF   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-00350978.
XX
PR   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI   Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI   Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR   WPI; 2003-450961/43.
DR   P-PSDB; ADB64489.
XX
PT   New polynucleotides and polypeptides, useful for developing a diagnostic
PT   marker or medicines for regulation of their expression and activity, or
PT   as targets of gene therapy.
XX
PS   Claim 1; Page; 222pp; English.
XX
CC   The invention discloses a polynucleotide comprising a sequence selected
CC   from 1970 fully defined nucleotide sequences which encode novel
CC   polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC   or its partial peptide, an antibody binding to the polypeptide or peptide
CC   of the polynucleotide, immunologically assaying the polypeptide or
CC   peptide of the polynucleotide by contacting the polypeptide or peptide
CC   with the antibody of the encoded protein, and observing the binding
CC   between the two, a transformant carrying the polynucleotide in an
CC   expressible manner and an antisense polynucleotide. The oligonucleotide
CC   is useful as a primer for synthesising the polynucleotide, or as a probe
CC   for detecting the polynucleotide. The polynucleotides and encoded
CC   proteins are useful as pharmaceutical agents and many disease-related
CC   genes may be included in them, for developing a diagnostic marker or
CC   medicines for regulation of their expression and activity, or as targets
CC   of gene therapy. The genes are involved in tissue and/or cell
CC   regeneration. Membrane proteins, signal transduction-related proteins,
CC   transcription-related proteins, disease-related proteins and genes
CC   encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC   neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC   the activity or expression of the encoded protein to treat diseases. The
CC   sequence presented is a cDNA of the invention. Note: Some of the sequence
CC   data for this patent is not represented in the printed specification, but
CC   is based on sequence information supplied by the European Patent Office.
XX
SQ   Sequence 1925 BP; 579 A; 441 C; 498 G; 407 T; 0 U; 0 Other;
```

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Query Match             48.9%;  Score 1266.4;  DB 10;  Length 1925;
Best Local Similarity   82.0%;
Matches  1571;  Conservative    0;  Mismatches  301;  Indels  44;  Gaps   8;

Qy   66 GGGACACGGCAAGGAAATGAGCAACTTCTCTGAATTACAAAGTCTTTCTCCAAAGAGCAGCAGA 125
         ||||| || || || ||||||| |||| || |||||||||| ||||| ||||||| ||||||||
Db   33 GGGACAGCGAGGAGATGAGCGCCATCCTTCTGAATTACAAATCTTTTTCCAAAGCAGCAGCAGA 92

Qy  126 CCATGGATAACTTGGAAAAGCAAACTGATCTGTCCATCTGCCTAGAGATGTTCACGAAGC 185
         ||||||||||||| || ||| ||||| |||| || ||||||||||||||||||||||| |
Db   93 CCATGGATAACTTAGAGAAGGCAAACTCATCTGTTCCCATCTGCCTTAGAGATGTTCACGAAAC 152

Qy  186 CTGTGGTCATTCTCCTTGCCAGCACAACCTGTTGCAGGAAAATGTGCCAGTGACATCTTCC 245
         ||||||| |||||| ||| |||||||||||| | |||||||||||||||||||| || ||||
Db  153 CTGTGGTGATTCTCCCTTGTCAGCACAACCTGTGTGAGGAAAATGTGCCAGTGATATTTCC 212

Qy  246 AGGGCCTCTAACCCGTTACTTACCCACAAGAGGAGGGCACCACCGTGCCATCAGGGGCCGCT 305
         || ||||||||||||| | ||| ||||||||||||| |||||| ||| ||||||||| ||  |
Db  213 AGGCCTCTAACCCGTATTTGCCCACAAGAGGAGGGTACCACCCATGGCCATCAGGGGCGCGAT 272

Qy  306 TCCGCTGTCCCTCCTGCAGACATGAGGTGGGTCTTGTTAGACAGACATGGGGGTCTTATGGACTGC 365
         ||||||| ||| ||  | ||||||| ||||   |||  || |||||||||||| | |||||||| |
Db  273 TCCGCTGCCCATCCGTGTAGACATGAAGTGGTTTGGATGTAGACATGGGGGTATATGGACTTC 332
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Qy   366 AGAGGAACCTGCTCGTTGGGAAAACATTATTGATATCTTACACAGCAGGAATCCACCAGCCAG 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 AGAGGAACCCTGCTCGGTGGGAAAAATATCATTGACATCTTACACAGCAGGAGTCCACCAGCCAG 392

Qy   426 AAAAAAAATTGGACCAGCCCATGTGTGAGAGAGACAGGAGGAACCCATCAACATCTATT 485
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Db   393 AAAAGAAAATCCGACACCAGCCCATGTGCGAGAGAACATGAAGAGGAGCCCATCAACATCTACT 452

Qy   486 GTCTGAACTGTGAAGTGCCCAACGCCCCAATAAGGACT 545
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Db   453 GTCTGAACTCGGAAGTACCCAAGGCGGTGCACACAAGACT 512

Qy   546 GCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGGCCAGAGACTCAGTGATGGTA 605
          ||||||||||||||||||||||||||||||||||||||||||
Db   513 GCCAGGTGGCTCCCCTCCACTCATGTGTTCCAGAGAGTCTGAGCCTCAGTGATGGCA 572

Qy   606 TTGCTGTACTTGTGGAAGCAACGATAGAGTGTGTGGCCAGAGCCAGCCTGGAGGACA 665
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Db   573 TCGCCAATCCTGGGCGCAGCAAACGATCGAGTCCAGGAGTCCAGCCAGCTGGGAAGACA 632

Qy   666 CCTGTAAAACTATTGAGGAGTGCTGCAGAAAGCAGAAACAGGACTGTGTGTGAGAAATTTG 725
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Db   633 CCTGCAAAACTATCGAGGAATGTTGCAGAAATGACCAAGCCATCACACTCGAA 692

Qy   726 ATCACCTATACGGCATCCTGAGGAGGAGGAGGAACTGAACTGACCAAGCCATCACTCGA 785
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Db   693 ATTACCTGTATGGCATTTGGAGCAACGAGAGCCAGAGAAATGACCCAAGTCAGTTGATGGCA 752

Qy   786 CACAGAGGAGGAAACTGGAACATGGCAGCATGTCCGGAACTCTTATTCAGGAAGAGTATTCCGGATCACCTGG 845
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Db   753 CCCAAGAGGAGAAACTCGGAACATGTCCGTGCTCTGATCAAAAAGTATTCTGATCATTTGG 812

Qy   846 AGAACGTATCCAAGTTGGTGGTGGTCAGAGAATCCAGTTCAGTTCATGGATGAGCCCGAAATGGCAG 905
          ||||||||||||||||||||||||||||||||||||||||||
Db   813 AGAACGTCTCAAAGTTGGTTGGTTGAGTCAGGAATTCAGTTTATGGATGAGCCCAGAAATGCAG 872

Qy   906 TATTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGCGTTTC 965
          ||||||||||||||||||||||||||||||||||||||||||
Db   873 TGTTTCTGCAGAAATGCCAAAACCCTGCTAAAAAAATCTCGGGAAGCCATCAAAGGGCATTTC 932

Qy   966 AGATGAGAGAACTAGAACAAGGTTTATGGAGATCATGAGGACGAACTTCACTCTGTCAATCTCAATA 1025
          ||||||||||||||||||||||||||||||||||||||||||
Db   933 AGATGAGAAAATAGAACATGGCTATGAGGAACCACTTCACAGTCAACCTCAATA 992

Qy   1026 GAGAGAGAAAAATTATCCGTGAAAATTGACTTTTTCTAGAGAAGAGAGGAGGAGAAGATG 1085
          ||||||||||||||||||||||||||||||||||||||||||
Db   993 GAGAGAAAAAGAATAATACGTGAAAATTGACTTTTACAGAGGAAGATGAGAAGAAGAAGAAG 1052

Qy   1086 CAGGAGAAATAGATGAAGAAGGAGGAGAGA-------------GGATGCAGTAGAAG 1130
          |||||||||||||||||||||||||||| ||||||||||
Db   1053 AAGGAGGCGGAGAAGAAGGGGAGGAGGAAGAGGGGAAGTGGGGAGGAGAACGGAGTAGAAG 1112

Qy   1131 TAGAGGAGGGAGAGAAAATTGTTCAAATAGCATCTTCNGGCGGGAAGAGGTCTGGAGAAG 1190
          ||||||||||||||||||||||||||||||||||||||||||
Db   1113 TGGAAGAGGTAGAAAACGTTCAAACAGCATCCCAGTGCCTCTGAAAAACCCAGAGAAAAG 1172

Qy   1191 CTGCAGAGAGCCCTCTCAGCTTCCCGCGACGCTTCGCGCCCAGAGAGCCCACTACCTGCTT 1250
          ||||||||||||||||||||||||||||||||||||||||||
Db   1173 CTTCAGAGCTCTCAG------GTCGGAGCTGCAGGCGTGCCCCTGCGGGGGGCACTTCCAGTT 1226

Qy   1251 CCTCTCCAGAACCGTTTTCATCCATGCCACCTGCTGCGAGATGTCCTGTGACACAGCGGGG 1310
          ||||||||||||||||||||||||||||||||||||||||||
Db   1227 CCTCTCCAGAGCCCCCCCACTTCCACTCCGCTGCTCTGGGATGTCCCCTGTGACACAGGGGG 1286

Qy   1311 AGGTTGTGCCCATTTGGCTCTCAGCGACCACAGTCTGAAACTTCAGCGCCTTCAGCAG 1370
          ||||||||||||||||||||||||||||||||||||||||||
Db   1287 AGGTTGTACCCACTGGCTCTGAGCGACCACAGAGTCTGAAACTCCAGTGCCTCTGCAGCG 1346

Qy   1371 CGGAAAACTGCGGGATCCCTTGTTTTACCCTAGTTGGTATAAAGGCCAAAGCGGGAAAACCA 1430
          ||||||||||||||||||||||||||||||||||||||||||
Db   1347 CAGAAACTGCGGGATCCCTTGTTTTACCCTAGTTGGTATAAAGGCCAAACCCGGGAAAAGCCA 1406

Qy   1431 GCTCCAACCCACCTTGCACTCATGGGGAGTGAAGGGTCAAAATAGGGCTCTGGGCA 1490
          ||||||||||||||||||||||||||||||||||||||||||
Db   1407 CCACCAACCCACCTTGCACCCCCAGGGGAGGCGGAAAGGGTCTGGGGGGCAAATGACCAGGGCAGCAG 1466

Qy   1491 TTGAGGATTCCAGTGTTGCAGTCCGCAGAGGTGGCAGCGAGAGCCGCAAGAAGGAGGT 1550
          ||||||||||||||||||||||||||||||||||||||||||
Db   1467 CTGAGGATTCGAATGTACGGAAGGCAGGAGAAGTGGCAGCCAGCGGGAAGCGGAGCAG 1526

Qy   1551 CAGTGAGTGTGGTTAAGGAGTCTTAGTTCAAACTGCAGCTACCTTCCAGATTGCATTGGAGGCCC 1610
          ||||||||||||||||||||||||||||||||||||||||||
Db   1527 CTGTGAGTGGGTAAGGAAAACTAGTGCACCTGCGACTACTTCTCAGATTGGAGGCTC 1586

Qy   1611 CTTCTCCCCAGGGACAGCTGTCCAGCCGCCTTGGGGGGTGGGGTGGG-GGTGATCCTGAGCCAG 1669
          ||||||||||||||||||||||||||||||||||||||||||
Db   1587 CTCCCCTTCCAGGGACAGGCTGCCAGCTCCAGCGGGAGCTGGGGAGGCTGAGTGGATCCTGAGCCAG 1646

Qy   1670 CTCGCCACGTCTCTTCCTTTCTCCTCTTGGTTTGAAATTCCCTAAATGAATTAATATTATTCTCG 1729
          ||||||||||||||||||||||||||||||||||||||||||
Db   1647 CTCGCCAATATCTTCTTCTTTTCCTGG--TTGAACTCCCTAAAGTGAATGAATATTCATTCCAA 1705

Qy   1730 TTGCCTGCCCCC--CTGTCTGCCCTGGCTCGAAAAGCACATAGGCAGCAGCAGGAAACAGGTGGAAT 1788
          ||||||||||||||||||||||||||||||||||||||||||
Db   1706 CTGCTGCCCCTCTGCTGTGAGATCGCATGTGGGGCAGCAGGCCCAAGTCAAA 1765

Qy   1789 TCACCACGATTCA---TATGAAGGGGGACCCTGGGACAGGGATTTCTGAAAAGCAAAAACAAAA 1845
          ||||||||||||||||||||||||||||||||||||||||||
Db   1766 TTAAATATTATGCAGATGATGAAAGGGGACACCTCTGAACAGGGGATTTCTGCA-------------- 1813

Qy   1846 CAAATACAACACCACCACCCTTTAATTCCAGATGACTTATCTCAC-TCATTGAGAAAATGA 1904
          ||||||||||||||||||||||||||||||||||||||||||
Db   1814 ----AAAATAGCCCAAACTGCAATTCCATATGACTTTATCTTGGGGGTGGAAAGA 1869

Qy   1905 TTTATGCTCAGAACAAAAATTACAGAAAAAATATACTCTTCTGAAGAAAACTTGATCTTCTGC 1960
          ||||||||||||||||||||||||||||||||||||||||||
Db   1870 ATATTTTGAGAAAAATAGTTGCAGAAAGCACTCGGAAAATAATAAAACTTGATCTTTATAC 1925

PI Hafalia AJA, Tang TY, Khan FA, Ison CH, Baughn MR;
PI Warren BA, Duggan BM, Thangavelu K, Honchell CD, Azimzai Y;
PI Elliott VS, Burford N, Ding L, Yue H, Becha S, Emerling BM;
PI Richardson TW, Lee SY, Bandman O, Lal PG, Lee S, Gietzen KJ;
PI Walia NK, Griffin JA, Lee EA, Swarnakar A, Ring HZ, Jones KA;
XX
DR WPI; 2003-092894/08.
DR P-PSDB; AAE32110.
XX
PT New human cytoskeleton-associated proteins, useful for preparing a
PT composition for diagnosing or treating a disease or condition associated
PT with decreased expression or overexpression of functional CSAP e.g.,
PT cancer.
XX
PS Claim 5; Page 211-212; 233pp; English.
XX
CC The invention relates to new human cytoskeleton-associated protein (CSAP)
CC and its polynucleotide. The polypeptide is useful for preparing a
CC composition for diagnosing or treating a disease or condition associated
CC with decreased expression or overexpression of functional CSAP e.g.
CC atherosclerosis or cancer. The present sequence is human CSAP-8 cDNA. The
CC invention is useful in gene therapy
XX
SQ Sequence 2434 BP; 753 A; 511 C; 553 G; 617 T; 0 U; 0 Other;

Query Match   35.2%; Score 910.8; DB 8; Length 2434;
Best Local Similarity   84.2%; Pred. No. 1e-231;
Matches 1058; Conservative   0; Mismatches 177; Indels   21; Gaps   2;

Qy   66 GGGACAGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCCAAAGAGAGCAGCAGA 125
           |||||| ||| |||||||||||| |||||| |||||||||| |||||| ||||||||||| |||||
Db   170 GGGACAGCAGGAGGATGAGCGGCATCTCTGAAATTACAAATCTTTTTCCAAAGAGCAGCAGAGA 229

Qy   126 CCATGGGATAACTTAGGAGAAAAGCAACTACTGATCTGTATCCCATCTGCCTAGAGATGTTCACGAAGC 185
           ||||| ||| |||||||||||| |||||||||||||||||||||||||| ||||||||||||| ||||||
Db   230 CCATGGGATAACTTAGAGAAGCCAACTCATCGTGTCCCATCTGCCTTAGAGATGTTCACGAAAC 289

Qy   186 CTGTGGTCATTCTCCCTTGCCAGACAACCTGTGCGAGAGAAATGTGCCAGTGACATCTTCC 245
           |||||||||||||| ||||||||| |||||||||||||||| ||||||||||||||| ||||
Db   290 CTGTGGGTGATTCTCCCTTGTCAGACAACCTGTGTAGGAGAAATGTGCCAGTGACATGTTTCC 349

Qy   246 AGGGCCTCTAACCCGTACTTACCCACGTGGCATCAGGGGGGGCCGCT 305
           ||||| ||||||||||| ||| ||| ||||||||||||||||| ||||
Db   350 AGGGCCTCTAACCCGTATTTGCCCACAGAGGAGGTTACCACCATCAGGGGGCCGAT 409

Qy   306 TCCGCGTCCCTCCTCCGCAGACATGAGGTGGTGTTAGACAGACAATGGGGGTCTATGGACTTGC 365
           ||||| |||||||||||||||||||||| |||||||||||||||||||| |||||||||||||||
Db   410 TCCGGCTGCCCATCCTGTAGACATGAGTGGTTTTGGATAGACATGGGGTATATCGGACTTTC 469

Qy   366 AGAGGAACCTGCTCGTGGGAAAAACAATTATTGATAATCTACAAGCAGGAATCCACCAGGCCAG 425
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Db   470 AGAGGAACCTGCTCGTGGTGGAAAAATATCATTGACACTACAAGCCAGGAATCCACCAGGCCAG 529

Qy   426 AAAAGAAAATTGGACCAGCCCATTGTGTGAAGAGGAACGCATCAAACATCTATT 485
           ||||||||| |||||||||||||| |||||||||||| ||| |||||||||||||
Db   530 AAAAGAAAATCCGACCACCATGTGCGAGAGAACAATGAAACATCTCTACT 589

Qy   486 GTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGTGCAAGGTTTTTTGGCGCCCATAAGGACT 545
           |||||||||| |||||||||||||||| |||| |||||||||| |||| |||||||||||||||
Db   590 GTCTGAACTGCGAAGTACCCACCTGCTCTGTGTTGCAAGGGTGTTTTGGTTGCGCCCATAAGGACT 649

Qy   546 GCCAGGTGGTCCCCTGACTCATGTGTTCCAGAGGCAAGAGTCAGAGCTCAGTGTGATGGTA 605
           ||||| |||||||||||| | |||||||||||||| ||||||||||||| |||||||||||||
Db   650 GCCAGGTGGCTCCCCTCACTCATGTGTTCCAGAGGACAGAGAGTCTGAGCTCAGTGATGGGCA 709

Qy   606 TTGCTGTACTTGTGGGAAGCAACGATAGAGCCAGGGTTGTGTCAGCTGGGACCA 665
           ||| |||||||||| ||||||||||||||||||||||||||| ||| ||| |||||
Db   710 TCGCCCATCCTCGTGGGCAGCAGCGAATCGAGTCCAGGGAGTGATCAGCCGGAAGACA 769

Qy   666 CCTGTAAAACTATTGAGGAGTGCTCGCAGAAAGCAGGACTTGTGTTGAGAAATTTG 725
           ||||| |||| |||||||||||||| |||||| ||||||||| |||||||||| ||||
Db   770 CCTGCAAAACTATCGAGGAATGTTGCAGAAAACAGAAAACAAGAGCTTTGTGAGAAGTTTG 829

Qy   726 ATCACCTATACGGCATCCTCGGAGTGAGGAGCGAAGACTGAAAATGACCCAAGCCATCACTCGAA 785
           |||| |||| |||||| ||| |||||||||||| |||||||||| |||||| ||| |||||||||||
Db   830 ATTACCTGTATCGGCATTTTGGAGCAGAAGAGCCAAGTGAAAATGACCCAAGTCATTACCCGAA 889

Qy   786 CACAGGAGGAGGAAAACTGGAACACTGGACATGTCCGGAACTCTTATCGGAGGTATTCCGATCATTGG 845
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Db   890 CCCAAGAGGAGGAAAAACTGGAACACATGTCCGGAACTCCTTATCGGAGGTTTCTGGATCATTTGG 949

Qy   846 AGAACGTATCCAAGTTGGTGGAGTGCAGGAATCCAGTTCATGGAGTGAGCCCGAAATGGCAG 905
           ||||| ||| |||||||||||||||| |||||||||||||| ||||||||| |||||||||| |||
Db   950 AGAACGTCTCAAAGTTGGTTGAGTCAGGAAATTCAGTTTATGAGGATTGATGAGCCAGAAAATGGCAG 1009

Qy   906 TATTTCTGCAGAATGCCAGAACCCTGCTCAAAAACCCTGTTGCCAAAAGAGATCGTTGGAGTGAGTTTC 965
           ||||||||||||||||| |||| |||||| ||||| ||||||||||||||| |||| |||||||| ||||
Db   1010 TGTTTCTGCAGAATGCCAGAACCCTGCTCAAAAACTCTGGAGCCATCAAAAGGCGTTTC 1069

Qy   966 AGAGTGGAGAAAACTAGAACCAAGGTTTATGAGTCATCATGAGCAACTTCACTGTCAATCTCAATA 1025
           ||||| |||||||| |||||||| |||| |||| |||| ||||||| |||||| |||| ||||| |||
Db   1070 AGATGCAGAGAAAATAGAACAATAGCATCTCAGGGAGGAGAAGTTGGAGAGAAGAGGAAGAGTTCTGAA 1129

Qy   1026 GAGAGAGAAAAAATTATCCGTGAAAATTGACTTTTCTAGAGAGAAGAGAGAGAGAAGAGAGATG 1085
           |||||||||| ||||| ||| ||||||||||||||| ||||||||||||||| |||||||| |||
Db   1130 GAGAGAGAAAAGATAATAATCACGTTGAAAATTGACTTTTACAGAGAAGAAGAGAGAAGAGAAG 1189

Qy   1086 CAGGAGAAATAGATGAAGAAGAGGAGAAAGGAGA----------------GGATGCAGTAGAAG 1130
           |||||||| ||||| ||||| |||||| |||||| |||||||||| |||
Db   1190 AAGAAGGCGAGAAGGAGAAAAGGAGAAGTGGGAGGAAGCAGTTGAGAAG 1249

Qy   1131 TAGAAGAGGGCAGAAAGAAGTTCAAATAGCATCTCAGGGGGAGGAAGAGTCTGGAGAAAG 1190
           ||||| |||||| ||| |||||||||| |||||||| ||| ||||||||| ||||||||||
Db   1250 TGGAAAGAGGTTAGAAAAATGTTCAAACAGAGTTTCCAGGAGAATGAAAACACCCAGAAAAAG 1309

Qy   1191 CTGCAGAGGCCCTCTCAGCTTTCCCGCAGAAGCTTCAGGTCGCCCAGAGCCACTACCTGCTT 1250
           ||||||||||| | ||||| |||||| |||||| ||||| |||||| ||| |||| |||||||
Db   1310 CTTCAGGAGCTCTTCAGGTGGGAGCTGCAGGCTGCCCCGGGGCACTTCCAGTTT 1363

Qy   1251 CCTCTTCCAGAACCGTTTTCATCCATTGCCACCTTGCTGCAGATGTCCTTGGCACACAG 1306
           ||||||||||| |||||| |||||||||| |||||| |||||| ||||| |||||||||
Db   1364 CCTCTTCCAGACGCCACCTTCCAGCCCTGCCGGATGCCCCTGTCACACAG 1419

Db   Sequence 2434 BP; 753 A; 511 C; 553 G; 617 T; 0 U; 0 Other;

RESULT 4
ADB62279
ID   ADB62279 standard; cDNA; 2634 BP.
XX
AC   ADB62279;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human cDNA encoding clone DFNES20073320.
XX
KW   Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW   tissue regeneration; cell regeneration; membrane protein;
KW   signal transduction-related protein; transcription-related protein;
KW   osteoporosis; neurological disease; cancer; tumour.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   377..1735
FT   /tag= a
FT   /product= "Clone DFNES20073320 protein"
XX
PN   EP1308459-A2.
XX
PD   07-MAY-2003.
XX
PF   28-MAR-2002; 2002EP-00007401.
XX
PR   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-00350978.
XX
PA   (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai R, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR P-PSDB; ADB64249.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The genes are involved in
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.
XX
SQ Sequence 2634 BP; 793 A; 580 C; 586 G; 675 T; 0 U; 0 Other;

Query Match   35.2%; Score 910.8; DB 10; Length 2634;
Best Local Similarity   84.2%;
Matches 1058; Conservative   0; Pred. No. 1.1e-231; Mismatches 177; Indels 21; Gaps 2;

```
Qy    66 GGGACACGGCCAAGGAAATGAGCACTTCCTGAATTAACAAGTCTTTCTCCAAAGAGCAGCAGA 125
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Db   363 GGGGACAGCGAGGAGATGAGCGCATCCTGAATTACAAATCTTTTTTCCAAAGAGCAGCAGA 422

Qy   126 CCATGGATAACTTGGAAAAGCAAACTGATTCTGTCCCATCTGCCTAGAGATGTTCACGAAGC 185
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Db   423 CCATGGATAACTCATCTGTCCCATCTGCTTAGAGATGTTCACGAAAC 482

Qy   186 CTGTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGAGGAGAAAATGTGCCAGTGACACTTCC 245
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Db   483 CTGTGGTGATTCTCCCTTGTCAGCACAACCTGTGAGGAAAATGTGCCAGTGATATTTTCC 542

Qy   246 AGGGCCTCTAACCCGTACTTACCCAAGAGGAGCACCACCGTGGCATCAGGGGCCGCGCT 305
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Db   543 AGGGCCTCTAACCGTATTTGCCCAAGAGGAGGTCACCACCGTGGGGCATCAGGGGGCCCGAT 602

Qy   306 TCCGCTGTCTCCCTCCTCCAGACATGAGGTGGGTGTTAGACAGAGACAGACTGC 365
         ||||  ||| |||||||  || ||||||||||||||| || || |||||||||||
Db   603 TCGGCTGCCCAATCCTGTAGACATGAAGTGGTTTTGGATAAGACATGGGACTTC 662

Qy   366 AGAGGAAACCTGCTCGTGGAAAACATTATTTACACGAGCAAGGAATCCACCAGGCCAC 425
         ||| |||||  | ||||||||| || ||||  ||||| |||  ||||||||||| ||||
Db   663 AGAGGAACCTCGTGGTGGAAAATATCATTGACATCTCACAAGCAGAGTCCACCAGGCCAG 722

Qy   426 AAAAAAAATTGGACACAGCCCATGTGTGAAGAGCATGAAGAGGAGAACATCAACATCTTATT 485
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Db   723 AAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGAGGAGCCATCAACATCTACT 782

Db   783 GTCTGAACTGCGGAGGTACCCACCCTGCTTCTTTTGTGCAAGGGTGTTGGTGCACAAAGACT 842

Qy   486 GTCTGAACTGTGAAGTGCCCACCCTGTTCCTTGTGCAAGGGTTTTGGCGCGCCATAAGGACT 545
         |||||||||| |||| |||||||||||||||||||||||||| ||||  |||  ||||||||
Db   843 GCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGCCAGAGAAGAAGTCTCAGGTGATGGCA 902

Qy   606 TTGCTGTTACTTGTGGGAGGCAACGATGAGAGTCCAGGGTGTGATCAGGCGACGGGAGGACA 665
         || ||| ||||||||| ||||| |||| |||| ||||| |||| ||| ||||| |||| |||
Db   903 TCGCCATCCTCGTGGGCAGCAACGATCGAGTCCAGGGTCTGATTAGGGAGA 962

Qy   666 CCTGTAAAAACTATTGAGGAGTGGCTGCAGAAAGCAGAGAAACAGGACCTGTGTGAGAAATTTG 725
         ||||||||| |||||||||||| ||||||||||||||||||||||||||| || |||||| |||
Db   963 CCTGCAAAAACTATCGAGGAATGGCTGCAGAAAGCAGAGAGACTTTTGTGAGAAGTTTC 1022

Qy   726 ATCACCTATACGGCATCCTGAGAGTGAAGGAGGACTGAAATGACCCAAGCCATCACTCGAA 785
         || || |||||||||||||||||||| ||||||| |||||||| || ||||| || |||||
Db  1023 ATTACCTGTACGGCATTTTGGACAGAAGAGAAGGAAATGACCCAAGTCATTACCCGAA 1082

Qy   786 CACAGAGGAGGAGAAAACTGGAACAATGTCCGAACTCTTATCAGGAATTCCGATCACCTGG 845
         ||||| ||||||| ||||| || ||| | |  ||| ||  || |||||  ||||| |||||
Db  1083 CCCAGAGGAGGAAACTGGAACAATGTCCGAGCTCTTATCAGGAATTTCAATCATCATTGG 1142

Qy   846 AGAACGTATCCAAGTTGGGTGGAGTCAGGAATCCAGTTGTCATGGATGAGCCCGAAATGGCAG 905
         ||||| |||||||||| || |||| ||||||||||| || ||||| || |||||||||||||
Db  1143 AGAACGTCTCAAAGTTCGTTGAGTCAGGAATTCAGTTATCAATGGATGAGCCAGAAATGGCAG 1202

Qy   906 TATTTCTGCAGAATGCCAAGACCCTGTTGCAAAGATCGGTGGAAGCATCAAAGGCGTTC 965
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Db  1203 TGTTTCTGCAGAATGCCAAAACCCTGCTAAAAAGGCATCAAAGAGCATCAGGCATTTC 1262

Qy   966 AGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACAACTTCACTGTGTCAATCTCAATA 1025
         || |||||||| ||| ||| | ||| ||| || || ||| ||||||| ||  |  ||||| |||
Db  1263 AGATGGAGAAATAGAACATGGCTAATGGAGAACATGGAAGTCAACACCTCAACTA 1322

Qy  1026 GAGAGAAAAAATTATCCGTGAAAATTGACACTTTTTCTAGAGAGAAGGAGGAGGAAGGAGAGATG 1085
         ||||| ||  | ||  |||||| || |||| ||||| || ||||||||| || |||||| |||
Db  1323 GAGAGAGAAGATAATACGTGAAAATTGACTTTTACGAGGAAGGAGGATGAAGATGAAGAGAG 1382

Qy  1086 CAGGAGAAATAGATGAAGAGGAGAAGGAGA----------------GGATGCCAGTGAGAAG 1130
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Db  1383 AAGAAGGCCGAGAAGGAGAAGGAGAAGAAAAGAGAGGGAGGGAGGAGCAGTAGGAGAAG 1442

Qy  1131 TAGAGAAGGGCAGAAATGTTCAAAATAGCACTTCAGGGGAGGAGAGGAGCTGGGAAGAAG 1190
         | || |||| |||||| || |||| | || ||||||| |||||| |||| |||| |||
Db  1443 TGGAAGAGGGTAGAAAAATGGTTCAAACAGAATTTCCAGGAGATGAAAACCCAGAAAAAG 1502

Qy  1191 CTGCAGAGCCCCTCTCAGCTTCCCGCAGAGCTTCAGGTGTCGCCCCAGAAGCCACTACCTGCTT 1250
         || |||||||| |||| ||| |||  | |||||||||||| |||||||||||||| |||||||
Db  1503 CTTCAGAGCTCTCTCAG------GTGGAGCTGCAGAGGCTGCCCCTGGGGGGCCCACTTCCAGTTT 1556

Qy  1251 CCTCTCCAGAACCGTTTTCATCCATGCCACCTGCTTCCAGATGTCCTGGTGACACAG 1306
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Db  1557 CCTCTCCAGAGCCCACCTCCAGCCCTGCCCACCCTGCCGGGATGCCCAGAGGATGAACACAG 1612
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RESULT 5
ADQ24315

ID   ADQ24315 standard; DNA; 2662 BP.
XX
AC   ADQ24315;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7135.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200404938-A2.

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XX
PD    10-JUN-2004.
XX
PF    26-NOV-2003; 2003WO-US038193.
XX
PR    26-NOV-2002; 2002US-0429739P.
XX
PA    (PROT-) PROTEIN DESIGN LABS INC.
XX
PI    Aziz N, Ginsburg WM, Zlotnik A;
XX
DR    WPI; 2004-441208/41.
XX
PT    Early detection of soft tissue sarcoma comprises determining expression
PT    of a gene in a first soft tissue sample and a normal soft tissue sample
PT    and comparing the gene expression, also useful in treating soft tissue
PT    sarcoma.
XX
PS    Example 2; SEQ ID NO 7135; 210pp; English.
XX
CC    The invention relates to a novel method for detecting soft tissue sarcoma
CC    which comprises obtaining a first soft tissue sample from an individual,
CC    and a normal soft tissue sample or different sample from the same or
CC    determining the expression of a gene in both samples and comparing the
CC    expression of the gene in both soft tissue samples, where a higher level
CC    of protein expression in the first soft tissue sample indicates the
CC    presence of soft tissue sarcoma. The method of the invention has
CC    cytostatic applications and may be useful for detecting soft tissue
CC    sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC    acid sequences may be useful in diagnostic and screening applications.
CC    The current sequence is that of a human soft tissue sarcoma-upregulated
CC    DNA of the invention. The current sequence is not shown within the
CC    specification per se but was submitted in CD format by the inventor.
XX
SQ    Sequence 2662 BP; 802 A; 587 C; 595 G; 678 T; 0 U; 0 Other;

Query Match             35.2%;  Score 910.8; DB 12;  Length 2662;
Best Local Similarity   84.2%;  Pred. No. 1.1e-231;
Matches 1058;  Conservative    0; Mismatches 177;  Indels   21; Gaps    2;

Qy       66 GGGACGGCCAAGGAAAATGAGACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGA 125
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Db       66 GGGGACAGGCGAGGAGATGAGCGGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGA 422

Qy      126 CCATGGATAACTTGGAAAAAGCAACTGATCTGCCTCGGATTACAATGTTTCCTAGGATGATGTTCACGAAGC 185
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Db      423 CCATGGATAACTTAGGAGAAGCAAACTCATCTGTCCCATCTGCCTAGAGATGTTCACGAAAC 482

Qy      186 CTGTGGGTCATTCTCCCTTGCCAGCACAACCTGTTGCAGGAAATGTGCCAGTGACATCTTCC 245
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      483 CTGTGGTGATTCTCCCTTGTCAGCACAACCTGTTGAGGAAATGTGCCCAGTGATATTTTCC 542

Qy      246 AGGGCCTCTAACCGTACTTACCCACACAAGAGGAGGAGGCACCACCGTGCCATCAGGGGCCGCT 305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      543 AGGGCCTCTAACCGTATTTGCCCACAAGAGGAGGGTACCACCGTGCCATCAGGGGCGCCGAT 602

Qy      306 TCCGGCTGTCCCTCCTGCAGACATCAGAGGTGGTTGTTAGACTGGGTCTATTGGACTGC 365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      603 TCCGGCTGCCCATCCTGTAGAGACATGAAGTGGTGTTTTGGGGATAGACATGGGGTTTGAATATGGGACTTC 662

Qy      366 AGAGGAACCTGCTGCTGGAAAAACAATTATTGATAATACTCAAGCAGCAGGAAATCCACCAGGGCCAG 425
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Db      663 AGAGGAACCTGGTGGTGGAAAATACATTCAAGCAGGAAGTCCACCAGGCCAG 722

Qy      426 AAAAAAAATTGGACCAGCCCATGTGTGAGAAGAGCAAGGCATCAACATCTATT 485
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Db      723 AAAAGAAATCCGACCACAGCCCATGTGCGACGAACATGAAGAGAGGAGGAAATCCACTTACT 782

Qy      486 GTCTGAACTGTGAAGTGCCCACCCTGTTCTTCGTGGCAAGGTTTTTGGCGCCCATAAGGACT 545
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Qy      546 GCCAGGTGGCTCCCTGACTCATGTGTTCCAGAGAGCAGAAGTCAGAGCTCAGTGATGGGTA 605
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      843 GCCAGGTGGGCTCCCTCACTCATGTGTTCCAGAGACAGAAGTCTGAGCTCAGTGATGGCA 902

Qy      606 TTGCTGTACTTGTGGGAAGCAACCATAGAGTTCCAGGGTTGGATCAGCCAGGGGAGGACA 665
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      903 TCGGCCATCCTCGGTGGGCAGCAACGATCGAGTCCCAGGGAGTCGATCAGCCAGGGGAGGACA 962

Qy      666 CCTGTAAAACTATTGAGGAGTGCTCCAGAAAAGACAGACAGGCAACCTGTGTGGAGAAATTTG 725
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Qy      786 CCCAACAGAGGAGGAGAACATGGGGACACATGTCCGTGCTCTGATCAAAAGTATTCTGATCATTGG 845
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Qy      846 AGAACGTATCCAAGTTGGGTGGAGTCAGGGAATCCAGTTCATGGAGGATGAGCCCGAAATGGCAG 905
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Qy      906 TATTTCTGCAGAATGCCAAGACCCGTGTTGCAAAGATCGTGGAAGCATCAAAAGGCCGTTTC 965
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Qy      966 AGATGGAGAAACTGAACAAGGTTATGAGGATCATGAGCAACTTCACTGTCAAATCCAATA 1025
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Qy     1026 GAGAGAGAAAAAATTATCCGTGAAATTGACTTTTCTAGAGAGGAGGAGGAAGGAGAAGAGATG 1085
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Db     1323 GAGAGAGAAAGATAATAACGTGAAAATTGACTTTTACAGAGAGGAGGAAGAGATGAAGAGAG 1382

Qy     1086 CAGGGAAAAATAGATGAAGAAGAAGAGGAAGAGGAGA---------------GGATGCAGTAGAAG 1130
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Db     1383 AAGAAGGCGGAGAAGGGAAGAGGAAGAGAAGAGAGAGAGGATGGGGAGGAGCAGTAGAAG 1442

Qy     1131 TAGAAGAGGGCAGAAAAATGTTCAAAAATAGCATCTTCAGGGGAGGAGGAGGAGGAGTCTGGAGAAG 1190
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Qy     1191 CTGCAGAGCCCCTCTCCAGCGTTCCCGGAGCGTTCAGGTGCCGCCCCAGCTACCTGCTT 1250
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Db     1503 CTTCAGAGCTGTCTCCAG--------GTGGGAGCTGCGCAGGGTGCCCCTGGGGGGCCACTTCCAGTTT 1556

Qy     1251 CCTCTCCAGAGACCGTTTCATCCATGCCACCTGCTGCGAGATGTCCTGGTGACACAG 1306
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Db     1557 CCTCTCCAGAGGCCACCTCCAGCCCTGCGGAGATGCCCCTGTCACACAG 1612
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RESULT 6
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ID    AAS25855 standard; cDNA; 1762 BP.
XX
AC    AAS25855;
XX
DT    07-NOV-2001  (first entry)
XX
DE    Human cDNA encoding a novel secreted protein, Seq ID 34.
XX
KW    Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW    cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW    antibacterial; virucide; fungicide; opthalmological; vulnerary;
KW    secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW    cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW    cerebral ischaemia; angiogenesis; nervous system disorder;
KW    Alzheimer's disease; infection; ocular disorder; corneal infection;
KW    wound healing; epithelial cell proliferation; skin ageing; food additive;
KW    preservative; antiproliferative.
XX
OS    Homo sapiens.
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PN   WO200155322-A2.
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PD   02-AUG-2001.
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PF   17-JAN-2001;  2001WO-US001341.
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PR   11-DEC-2000;  2000US-0540997P.
PR   05-JAN-2001;  2001US-0259678P.
XX
PA   (HUMA-)  HUMAN GENOME SCI INC.
XX
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PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-488783/53.
DR   P-PSDB; AAU15868.
XX
PT   New nucleic acid molecules encoding 461 human secreted proteins for
PT   diagnosing, preventing, treating or ameliorating medical conditions and
PT   used as food additives or preservatives.
XX
PS   Claim 1; SEQ ID NO 34; 980pp; English.
XX
CC   The invention relates to isolated nucleic acid molecules and their
CC   encoded secreted proteins. The nucleic acids and proteins are used to
CC   prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC   rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC   in diagnosing a pathological condition or susceptibility to a
CC   pathological condition. Antibodies to the proteins can also be used in
CC   alleviating symptoms associated with the disorders and in diagnostic
CC   immunoassays e.g. radioimmunoassay or enzyme linked immunosorbent assays
CC   (ELISA). Disorders which are diagnosed or treated include autoimmune
CC   diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC   neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC   arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC   nervous system disorders e.g. Alzheimer's disease, infections caused by
CC   bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC   and many other disorders listed in the specification. The polypeptides
CC   can also be used to aid wound healing and epithelial cell proliferation,
CC   to prevent skin aging due to sunburn, to maintain organs before
CC   transplantation, for supporting cell culture of primary tissues, to
CC   regenerate tissues and in chemotaxis. The polypeptides can also be used
CC   as a food additive or preservative to increase or decrease storage
CC   capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC   minerals, cofactors and other nutritional components. The present
CC   sequence encodes a novel secreted protein of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
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  Query Match     34.7%;  Score 899.8;  DB 4;  Length 1762;
  Best Local Similarity   84.2%;  Pred: No. 7.6e-229;
  Matches 1058; Conservative   0; Mismatches 177; Indels  22;  Gaps   3;

Qy          66 GGGACAGGCGAAGGAAATGAGGCACTTCTCTGAATTACAGAGTTTTCTCCAAAGAGCAGCAGA 125
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               ||||||||||||| |||||||||||||| |||| |||| |||||||||||||||||||| |
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Qy         186 CTGTGGGT-CATTCTCCCCTTGCCACACACACCTGTGCAGAAAATGTGCCAGTGACATCTTC 244
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Qy         245 CAGGCCTCTAACCCGTACTTACCCACAAGAGGAGGAGGCACCACCGTGGCATCAGGGGCCGC 304
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Qy         305 TTCCCGTGTCCTCCTGCAGCACATCAGGTCGTGTTTAGACAGACATGGGGTCTATCGGACTG 364
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Qy         365 CAGAGGGAACCTGCTCGTGGAAAAACATTATTGATTATTCTCAAAGCAGGAATCCACCAGGCCA 424
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Db         563 TGTCTGAACTGCGAAGTACCCACCTGCTCTCGTGCAAGGTGTTTTTGGTGCCACAAAGAC 622

Qy         545 TGCCAGGTGGCTCCCTGACTCAGTGTCCAGAGGCAGAAGTCAGAGCTCAGTGCATGGT 604
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Db         623 TGCCAGGTGGCTCCCTGACTCAGTGTTCCAGAGGCAGAAGTCAGAGCTCAGTGCATGGC 682

Qy         605 ATTGCTGTACTTGTGGGAAGCAACGATAGAGTCCAGGGTGTGATCAGCCAGCTGGAGGAC 664
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Db         683 ATCGGCCATCCTGCTGGGCGAGCAACGGATCCAGGGTGTTCCAGGGAGTGATCAGCCAGGTGGAGAC 742

Qy         665 ACCTGTAAAAACTATTGAGGAGTGCTGCAGAAGAGCAGGAGACCTGTGTGAGAAATTT 724
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Qy         725 GATCACCTATACGGCCATCCTGGAGGAGGAGGAGACTGAAATGACCCAAGCCACTCGA 784
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Qy         845 GAGAACGTATCCAAGTTGGTGGAGAGTGCAGAAATCCAGTTCATGGAATCGGAAATGGCA 904
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RESULT 7
ABX73196
ID   ABX73196 standard; DNA; 1762 BP.
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AC   ABX73196;
XX
DT   18-MAR-2003  (first entry)
XX
DE   Human novel polynucleotide #24.
XX
KW   Human; gene; dej; neural disorder; immune system disorder; renal disorder;
KW   muscular disorder; respiratory disease; reproductive disorder;
KW   gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW   hyperproliferative disorder; inflammatory disease; allergic reaction;
KW   blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW   cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
KW   haemostatic; antiarteriosclerotic.
XX
OS   Homo sapiens.
XX
PN   US2002132753-A1.
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XX
PD    19-SEP-2002.
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PF    17-JAN-2001; 2001US-00764864.
XX
PR    31-JAN-2000; 2000US-0179065P.
PR    04-FEB-2000; 2000US-0180628P.
PR    28-JUN-2000; 2000US-0214886P.
PR    07-JUL-2000; 2000US-0216407P.
PR    07-JUL-2000; 2000US-0216880P.
PR    11-JUL-2000; 2000US-0217487P.
PR    11-JUL-2000; 2000US-0217496P.
PR    14-JUL-2000; 2000US-0218290P.
PR    26-JUL-2000; 2000US-0220963P.
PR    26-JUL-2000; 2000US-0220964P.
PR    14-AUG-2000; 2000US-0224518P.
PR    14-AUG-2000; 2000US-0224519P.
PR    14-AUG-2000; 2000US-0225267P.
PR    14-AUG-2000; 2000US-0225268P.
PR    14-AUG-2000; 2000US-0225270P.
PR    14-AUG-2000; 2000US-0225447P.
PR    14-AUG-2000; 2000US-0225757P.
PR    14-AUG-2000; 2000US-0225758P.
PR    22-AUG-2000; 2000US-0226868P.
PR    30-AUG-2000; 2000US-0228924P.
PR    01-SEP-2000; 2000US-0229287P.
PR    01-SEP-2000; 2000US-0229343P.
PR    01-SEP-2000; 2000US-0229344P.
PR    01-SEP-2000; 2000US-0229345P.
PR    05-SEP-2000; 2000US-0229509P.
PR    05-SEP-2000; 2000US-0229513P.
PR    08-SEP-2000; 2000US-0231413P.
PR    21-SEP-2000; 2000US-0234223P.
PR    21-SEP-2000; 2000US-0234474P.
PR    25-SEP-2000; 2000US-0234997P.
PR    27-SEP-2000; 2000US-0235834P.
PR    29-SEP-2000; 2000US-0236327P.
PR    29-SEP-2000; 2000US-0236367P.
PR    29-SEP-2000; 2000US-0236368P.
PR    29-SEP-2000; 2000US-0236369P.
PR    29-SEP-2000; 2000US-0236370P.
PR    02-OCT-2000; 2000US-0236802P.
PR    02-OCT-2000; 2000US-0237037P.
PR    02-OCT-2000; 2000US-0237038P.
PR    02-OCT-2000; 2000US-0237039P.
PR    02-OCT-2000; 2000US-0237040P.
PR    13-OCT-2000; 2000US-0239935P.
PR    20-OCT-2000; 2000US-0240960P.
PR    20-OCT-2000; 2000US-0241785P.
PR    20-OCT-2000; 2000US-0241809P.
PR    01-NOV-2000; 2000US-0244617P.
PR    17-NOV-2000; 2000US-0249299P.
PR    08-DEC-2000; 2000US-0251856P.
PR    08-DEC-2000; 2000US-0251868P.
PR    08-DEC-2000; 2000US-0251869P.
XX
CC    polynucleotides. The polypeptides and polynucleotides are useful in gene
CC    therapy for treating, inhibiting or preventing neural disorders, immune
CC    system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
CC    and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
CC    nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
CC    gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
CC    (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
CC    heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
CC    renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
CC    leukaemia), inflammatory diseases and conditions (e.g. septic shock,
CC    appendicitis), allergic reactions and conditions (e.g. asthma), blood
CC    related disorders (e.g. thrombosis, atherosclerosis and myocardial
CC    infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
CC    human novel polynucleotides of the invention
XX
SQ    Sequence 1762 BP; 552 A; 401 C; 434 G; 375 T; 0 U; 0 Other;
```

```
Query Match       34.7%;  Score 899.8;  DB 8;  Length 1762;
Best Local Similarity   84.2%;  Pred. No. 7.6e-229;
Matches 1058;  Conservative   0;  Mismatches 177;  Indels 22;  Gaps 3;
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Qy     66 GGGACGGCCAAGGAGAAATGAGCAACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGAGA 125
          |||||| ||||||||||| |||||| |||||||||||||  |||||| || |||||||||||||||
Db    143 GGGACAGCGAGGAGAGGAGCGCCATCCTCTGAATTACAAAATCTTTTTCCAAAGAGCAGCAGAGA 202

Qy    126 CCATGGATAACTTGGAAAAGCAACTGAACTGTTCTCCCATCTGCCTAGAGATGTTCACGAAGC 185
          |||||| ||||||||| |||| || ||||||||| || |||||||| ||||||| |||||||||
Db    203 CCATGGATAACTTAGAGAAGGCAACTCATCTGTCCCATCTCGCTTAGAGATGTTCACGAAAC 262

Qy    186 CTGTGGT-CATTCTCCCTTGCCAGCACAACCTGTTGCAGGAAATGTCCAGTGACACTTC 244
          ||| ||| |||||||| ||||||||||||||||||||||| |||||||||||||||| ||
Db    263 CTGTGGTAGATTCTCCCTTGTCAGCACAACCTGTTGGAAATGTGCCAGTGATATTTTC 322

Qy    245 CAGGCCTCTAACCCGTACTTACCCACAACAAGAGGACCACCACCGGTGGCATCAGGGGCCGC 304
          |||||||||| ||||  ||| ||||||||||||||||| |||||||| ||||||||||||||
Db    323 CAGGCCTTCAACCCGTATTTGCCCACAACAAGAGGAGGTTACCCACCACCTGCCATCAGGGGCCGA 382

Qy    305 TTCCGCTGTCCCCTCCTCTGCGGACACGAGGTGGTTGTTAGACAGACAGCATGGGGGTCTTATGGACTG 364
          ||||||||||| ||||||||| |||||  ||||||||| ||||||| ||| ||||||||||||| ||||
Db    383 TTCCGCTGTGCCCATCCTGTAGACACATGAAGTTTTTGGATAGACACATGGGGGTATATGGAACTT 442

Qy    365 CAGAGGAAACCTGCTTCCTGTGGAAAACACTTATTGATAATATCTACAAGCACCACCAGGCCA 424
          ||||| |||||||||  |||||||| |||||||| |||||||| ||||||| ||||||||||
Db    443 CAGAGGAAACCTGCTGGTTGGAAAATATCATTGACATCTACAACCAGGACTCACCAGGCCA 502

Qy    425 GAAAAAAAAATTGGACCAGCCCATGTGTCGAAGCAGCATGAAGCATCAAACATCTAT 484
          ||||   |||  | ||||||||| || || ||||| |||||| ||||||||||||||
Db    503 GAAAAGAAATCCGACCCATGTGCGAGGAAACATGAAGCAGCGGCCATCAAACATCTAC 562

Qy    485 TGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGTGCAAGGTTTTTGGCGCCCCATAGGAC 544
          ||||||||||| |||  |||||| |||||||| |||||||| ||||| |||||||||  |||
Db    563 TGTCTGAACTGCGAAGTACCCACCTGCTCTCTGTGCAAGGTGTTGGTGCACACAAAGAC 622

Qy    545 TGCCAGTGGCTCCCCTGACTCATGTGTTCCAGAGGACAGAGAAGTCTGAGCTCAGTGATGGC 604
          ||||||||| |||||| ||||||||||| |||||| |||| || |||| |||||||||| ||
Db    605 ATCGCCATCCTCGTGGGCGCAACGATCAGGGGGTGTGATCAGCCAGCCTGGAAGAC 664

Qy    605 ATTGCTGTACTTGTGGGAAGCGAACGATAGAGTCCAGGGTGTGATCAGCCAGCCTGGAAGAC 664
          ||||| |||||||||||||| |||| || |  || ||||||||||||| |||||||  ||||
Db    665 ACCTGTAAAACTATTGAGAGGAGTGCTGCAGAAGCAGAAACAGGAACCTGTGTGTGAGAAATTT 724

Qy    665 ACCTGTAAAACTATTGAGAGGAGTGCTGCAGAAGCAGAAACAGGAACCTGTGTGTGAGAAATTT 724
          |||| |||||||| |||||||||||||||| |||||||||||||||| |||||||| ||||||
Db    725 GATCACCTATACGGGCCATCCTGGAGGAGGAGAAGATGAAATGACCCAAGCCCATCACTCGA 784

Qy    725 GATCACCTATACGGGCATCCCGTGGGACGAGGAGAAGATGAAATGACCCAAGCCCATCACTCGA 784
          |||| ||||||||||||| || |||||||||||||||||||||||||||||||||||||||||
Db    803 GATTACCTGTATGGCATTTGGAGGAAGAGGAAGAATGAAATGAAATGACCCAAGTCATTACCCGA 862

Qy    785 ACACAGGAGGAGAAACTGGAACATGTCCGAACTCTTATCAGGAAGTGTATTCCGATCACCTG 844
          | ||| |||||||| | |||||| | |  |||| |||| |||||| ||||||  |||||||
Db    863 ACCAAGAGGAGAAACTGGAACATGTCCGGTGCTCTCGGATCAAAAAAGTGATTATTCTGATCATTTG 922
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XX
PN    WPI; 2003-147444/14.
DR    P-PSDB; ABU54936.
XX
PI    Rosen CA, Ruben SM, Barash SC;
XX
PA    (ROSE/) ROSEN C A.
PA    (RUBE/) RUBEN S M.
PA    (BARA/) BARASH S C.
XX
PT    New polypeptides and nucleic acids, useful in gene therapy for treating,
PT    inhibiting or preventing e.g. neural, immune system, muscular,
PT    respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
PT    renal disorders.
XX
PS    Claim 1; SEQ ID NO 34; 402pp; English.
XX
CC    The invention relates to human novel polypeptides and their associated
```

Qy   845 GAGAACGTATCCAAGTTGGTTGGGAGTCAGAGTTCATGGATGGAGCCCGAAATGGCA 904
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   923 GAGAACGTCTCAAAGTTGGTTGAGTCAGGGAATTCAGTTTATGGATGAGCCGAAATGGCA 982

Qy   905 GTATTTCTGGAGGATGGCCAAGAACCTGTTCCAAAAGATCCTGTGGAAGCATCAAAGGCGTTT 964
          ||||||||||||| ||||| ||| ||||||
Db   983 GTGTTTCTGCAGAATGCCAAAAACCCTGCTAAAAAAATCTCAGAAGCATCAAAGGCACATTT 1042

Qy   965 CAGAATGGAGAAACTAGAACAAGAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCAAT 1024
          ||||| |||||| |||||||| |||||||||||| |||||||||| ||||||||
Db 1043 CAGATGCAGAAAATAGAACATGGCTATGAGAACAACCACTTCACAGTCAACCTCAAT 1102

Qy 1025 AGAGAAGAAAAAATTATCCCTGAAATTGACTTTCTAGAAGAAGAGGAAGAGAAAGAT 1084
          ||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 1103 AGAGAAGAAAAAGATAATAACGTTGAAATTGACTTTACAGAGAGAAGATGAAGAAGAGA 1162

Qy 1085 GCAGGAGAAATAGATGAAGGAAGGAAGAAGGAGA------------GGATGCAGTAGAA 1129
          |||||||||||||| ||| |||| ||||||||| || ||||||||
Db 1163 GAAGAAGGCGGAGAAGGAGGGAAGAAGAGAAGAAGGAGAAAGGAGAAGGCAGTAGAA 1222

Qy 1130 GTAGGAAGAGGCAGAAAATGTTCAAATAGCAATCTTCAGGGGAGAGGAGAGTCTGAGAAA 1189
          |||||||||||||||||||||||||||| |||||||||||||||||||||
Db 1223 GTGGAAGAGGTAGAAAATGTTCAAAACAGAGAGTTCCAGGAGAAGATGAAAAACCAGAAAAA 1282

Qy 1190 GCTCGCAGAGCCCTCTCAGCTTCCGCGCAGAGACTTCAGGTGCCCCAGAGCCCACTACCTGCT 1249
          |||||||||| ||| |||| ||||||||||||||||||||||||||
Db 1283 GCTTCAGAGCTCTTCTCAG------GTGGAGCTGCAGGCTGCCCCTGGGGGCACTTCCAGTT 1336

Qy 1250 TCCTTCTCCAGAACCGTTTTCATCCATGCCACCTGTCTGCAGATGTCCTGGTGACACAG 1306
          ||||||||||||| ||||||||||||||||||||||||||
Db 1337 TCCTCTCCAGAGCCACCTCGCTGCGGATGCCCCTGTGACACAG 1393

RESULT 8
ID   ADC30799 standard; cDNA; 1426 BP.
XX
AC   ADC30799;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human novel cDNA sequence, SEQ ID NO:881.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; chromosome 8q13; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200309271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI   Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI   Haley-Vicente D, Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC31770.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet

PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 881; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
CC   recombinant production of a polypeptide of the invention; an antibody
CC   against a polypeptide of the invention; a method of detecting
CC   polynucleotides or polypeptides of the invention; and methods of
CC   identifying a compound which binds to a polypeptide of the invention. The
CC   invention further discloses methods of preventing, treating or
CC   ameliorating a medical condition; kits comprising polynucleotide probes
CC   and/or monoclonal antibodies for carrying out the methods of the
CC   invention; methods for the identification of compounds that modulate the
CC   expression or activity of the polynucleotide and/or polypeptide; and
CC   contig sequences corresponding to the cDNA sequences of the invention
CC   (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC   -ADC33394). The nucleic acids and polypeptides of the invention are
CC   useful in diagnostics, drug screening, forensics, gene mapping, in the
CC   identification of mutations responsible for genetic disorders or other
CC   traits, for assessing biodiversity, and in producing many other types of
CC   data and products dependent on DNA and amino acid sequences. They are
CC   also used for treating diseases such as Parkinson's disease, Alzheimer's
CC   disease and other neurodegenerative diseases, anaemia, platelet
CC   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC   cancer. The nucleic acids may also be used as hybridisation probes or
CC   primers, and in the recombinant production of a protein. The polypeptides
CC   are also useful in generating antibodies, as molecular weight markers,
CC   and as food supplements. The present sequence represents a specifically
CC   claimed human cDNA sequence of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1426 BP; 448 A; 320 C; 365 G; 293 T; 0 U; 0 Other;

Query Match   32.5%; Score 841.2; DB 10; Length 1426;
Best Local Similarity   82.7%; Pred. No. 2.9e-213;
Matches 1012; Conservative   0; Mismatches 178; Indels 34; Gaps 3;

Qy   66 GGGACCGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTCTCCAAAGAGCAGCAGA 125
          |||| ||| |||||||||||||||||||||| ||||||||||||||||||
Db   120 GGGACAGCGAGGAGAATGAGCGCCATCTCTGAATTACAAAACTTTTCCAAAAGAGCAGCAGA 179

Qy   126 CCATCGGATAACTTGGAAAAAGCAAACTGATCTGTCTCCCATTCTCCCTAGAGATGTTCACGAAGC 185
          ||||||||| ||||||| ||| |||||||||||||||||||||||||||||||
Db   180 CCATCGGATAACTTACGAGAAGCAACTCATCGTCCCATCTCGCTTAGAGATGTTCACGAAAC 239

Qy   186 CTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACATCTTC- 244
          |||||||||||||||||||||||||||||| ||| |||| ||||||||||||||
Db   240 CTGTGGTGATTCTCCCTTGTCAGCAACACCTGTGTAGGAAATGTGCCAGTGGATATTTTCC 299

Qy   245 --------CAGGGCCTCTAACCCGTACTTACCCACAAGAGAGGACCACCACCGTGGCATCAG 296
                  |||||| |||||||||||||||||||||||||||||||||
Db   300 AGGTAGAACAGGGCCTCTAACCCGTATTTGCCACAAGAGGGTACCACCACCATGGCATCAG 359

Qy   297 GGGGCGCCGCTTCCGCTGTGTCCCTCCGCGAGACATGAGGTGGTGTTAGACAGACATGGGTCT 356
          |||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   360 GGGGCCGAGTTCCGCTGCCCATCCCTGTAGACATGAAGTGGTTTTTGATAGACATGGGTAT 419

Qy   357 ATGGACTGCAGAGGAACCTGCTGTGGAAAACATTATTGATATCTCACAGCAGGAATTCCA 416
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   420 ATGGACTTCAGAGGAACCTGCTGTGGAAAATATCATTGACATCTCACAAGCAGGAGTCCA 479

Qy   417 CCAGGCCAGAAAAAAAATTGGACCAGCCCATGTGTGGAAGAGACCATGAAGAGGACCGCATCA 476
          |||||||||||||||| |||||||||||||||||||||||||||||||
Db   480 CCAGGCCGAGAAAAGAAATCCGAACCAGCCCAGTGCGGAGGACACATGAAGAGGCGCATCA 539

Qy   477 ACATCTATTGTCTGAACTGTGAAGGTGCCCACCTGTTCCTGTGTCGCAAGGTTTTGGCGCCC 536

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RESULT 9
ABS70380
ID   ABS70380 standard; cDNA; 1757 BP.
XX
AC   ABS70380;
XX
DT   27-NOV-2002 (first entry)
XX
DE   Human bone remodelling gene #37.
XX
KW   Bone remodelling; osteoporosis; human; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US6426186-B1.
XX
PD   30-JUL-2002.
XX
PF   18-JAN-2000; 2000US-00484970.
XX
PR   18-JAN-2000; 2000US-00484970.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA, Volkmuth W, Walker MG;
XX
PT   A combination of polynucleotides which are co-expressed with genes known
PT   to be involved in bone remodelling and osteoporosis are useful in an array
PT   for the diagnosis of bone remodelling and osteoporosis associated
PT   disorders.
XX
PS   Claim 1; Col 135-138; 206pp; English.
XX
CC   The invention relates to a combination comprising a number of
CC   substantially purified and isolated polynucleotides which are co-
CC   expressed with genes known to be involved in bone remodelling and
CC   osteoporosis. The invention is used to diagnose disorders associated with
CC   bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
CC   remodelling genes of the invention
XX
SQ   Sequence 1757 BP; 473 A; 388 C; 513 G; 383 T; 0 U; 0 Other;

Query Match             18.7%;  Score 485.6; DB 6; Length 1757;
Best Local Similarity   67.7%;  Pred. No. 2.2e-118;
Matches  696; Conservative   0; Mismatches 329; Indels    3; Gaps    1;
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Qy    112 CAAAGAGCAGCAGACCATGCAATGAATAACTTGGAAAAAGCAACAACTGAATCTGTCCCATCTGCTAGA 171
          ||||||  |||||  |||||| ||| |||||||||||  |||  ||||||  |||||||||||||| ||
Db    148 CCAGGATGGGAATCCCATGGGAGAATCCCATGGGAGAAGCAGCTGAAATGCCCTATCTGCCTGGA 207

Qy    172 GATGTTCACGAAGCCTGTGGTCATTCTCCCGTTGGGAAGCAGCTGAAATGTGC 231
          ||||||||| |||||||||||  ||||||||||||||||||||||||||||||
Db    208 GATGTTACCAAGCCAGTGGGTCATCTCGCTGCCAGCACAACCTGCCGAAGTGTGC 267

Qy    232 CAGTGACATCTTCCAGCCTCTAACCCGTACTTACCCACAAGAGGAGGAGGAGGACGGTGGC 291
          ||||||||||||||  ||||||| ||||||||||||||||||||||||||||||||| ||
Db    268 CAATGATATTTTCCAGCCCTCTAAACCCGTATTTGCCCACAAGAGGAGGGTACCCACCATGGC 327

Qy    292 ATCAGGGGGCCGGCTTCCGGTGTCCCCTCCTCCAGACACATGAGGTGGGTGGTTAGACAGATCAGCATGG 351
          |||||||||||| |||||| |||||||||||||||| |||||||||||||||||  |||||||  |||||
Db    328 ATCAGGGGGCCCGATTCCGGCCGTCCCCATCCGTAGACAATGAACTGGGTTTTTGGATAGAGACATGG 387

Qy    352 GGTCTATGGACTGCGAGGAACCTGCTCGTGGAAAAACAATTATTGATATCTACAAGCAGGA 411
          |||||||||||| ||||||||||||||||||||||  |||||| |||||||||||||||||
Db    388 GGTATATGGGACTTCAGAGGAACCTGCTGGTGGGAAACATCATCAGACATCTACAAAACAGGA 447

Qy    412 ATCCACCA-----GGCAGAAAAAAATTGGACCCAGCCATGTGTGAAGACAGCATGAAGGA 468
          ||||||||     |||||||||||||||||| |||||||||||||||||||||||||||
Db    448 GTGCTCCAGTTCCTGCCGCCGCTGCAGAAGGGCAGTCACCCCATGTGCAAGGACGACGAAGATGA 507

Qy    469 ACGCACATCAAACATCTATTGTTCTGAAACTGTGAAGTGCCCACCTGTTCCTTGTTGTGCAAGGTTT 528
          |||||| |||  ||||  | ||| |||||||||||||||||||||||||| |||| |||||||||
Db    508 GAAAATCAACCATCTACTGTCTCACGTGCCCACGTGCCACCTGCTCCATGTGCAAGGTGT 567

Qy    529 TGGCGCCCCATAAGGACTGCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGCCAGAGAGTC 588
          ||||  ||| |||||||||||||||||||||||||||| ||  ||||||||||| ||||||||
Db    568 TGGGATCCACAAGGCCTGCGGGAGGTGCCCCCATTGCAGAGTGTCTTCCAGGGACAAAGAGAC 627

Qy    589 AGAGCTCAGTGATGTTATTGCTGTACTTGTGGGAAGCAACCGATAGAGTCCAGGGTGTGAT 648
          |||||||| | |||||||||||||||||||| ||||||||||||||| | |||||||||
Db    628 TGAACTGAATAACTGTATCTCCAAGTGCTGGTGGCGCGGGAATGACCCGTGTGCAGCCATCAT 687

Qy    649 CAGCCAGCCTGGAGGAGCACCTGTAAAACTATTGAGGAGAAAAGCAGAAAACAGGA 708
          ||||| ||| |||||| ||||| | ||||||||||||| ||| ||| |||| |||
Db    688 CACTCAGCTGAGGAATTCCCTCGACTGACCAAGAGAAGCAGTCACCAGGTAAAAGGAGAA 747

Qy    709 CCTGTGTGAGAAATTTGATCACCTATACGGGCATCCTGGAGGAGGAGGAAGACTGAAATGAC 768
          |||||||||||||||| |||  | ||||||| || |||||||||||||||
Db    768 [...]
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Upper alignment block (continued from prior page):

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Db    540 ACATCTTACTGTCTGAACTGCGAAGTACCACCTGCTCTCTGGTTGGTGCAC 599
          ||||  |||||||||||| ||||||||||||||||||||||||||||| |||
Qy    537 ATAAGGACTGCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGCCAGAGAGTCA 596

Db    600 ACAAAGACTGCGCAGGTGGCTCCCCTCACTCATGTGTTCCAGGGACAGAAGCTCA 659
          |||  | | ||| |||||| || ||||| |||||||||||||| | ||  ||||
Qy    597 GTGATGGTATTGCTGTACTTGTGGGAAGCAACGATAGAGTCGATCAGCCAGC 656

Db    660 GTGATGGCATGGCCATCCTCGTGGGCGCAGCAACGATGGGAGTGAGTCAGCCAGC 719
          ||||||| |||||||| || ||||| | |||||| |||| |||||| ||||||||
Qy    657 TGGAGGACACACCTGTAAAAACTATTGAGGAGTGCTGCAGAAGTATTCCG 716

Db    720 TTACCCGAACCCAAGAGGAGGAAACTGGAGGAAATGTTGCAGAAACAGAAAGAGCTTTGTG 779
          || ||||||| || ||||||| |||||| |||||||||||||||| ||| | ||||||||
Qy    717 AGAAAATTTGATCACCTATACGGCATCCTGGAGGAGGAGGAAGACTGAAATGACCCAAGCCA 776

Db    780 AGAAGTTTGATTACCTGTATGGCATTTTGGAGGAGGAGGAAGAAATGACCCAAGTCA 839
          ||||||||||| |||| | |||||| ||||||||||||||| |||||| ||||| ||
Qy    777 TCACTGGAACACAGGAGGAGAAACTGAACATGTCCAACTCTTATCGTGGAAGTATTCCG 836

Db    840 TTACCCGAACCCAAGAGGAGGAAACTGGACGAACATGTCCGTGTTCTTCAGTCAGGAATGA 899
          || ||||||| || ||||||| |||| |||||||||| | ||||| ||||| |||| ||
Qy    837 ATCACCTGGAGAAACGTATCCAAGTTCAGTTCACAGATGACGTGAAGTGCAGGTCAGGACCCG 896

Db    900 ATCATTTGGAGGAACGTCTCAAAGTTGGTTGAGTCAGGAATTCAGTTTATGGATGACCCAG 959
          ||||| |||||| ||||||| ||| |||||||||||||||||||| | ||  |||| ||||
Qy    897 AAAATGGCAGTATTTCTGGCAGAATGCCAAGACCCTGTTGTTGCAAAGATCGTTGGAAGCATCAA 956

Db    960 AAATGGCAGTGTTTCTGCGAATGCCAAAAACCCTGCTAAAAAAAAAAACTCGGAAGCATCAA 1019
          |||||||||| |||||| |||||||||||  |||||  ||||||||||| |||||||||||
Qy    957 AGGCGTTTCAGGATGGGGAGAACTAGAACAAGGTTATGAGCAACTTCACTGTCA 1016

Db   1020 AGGCATTTCAGAATGGCGGAGAAAATAGAACCACTTCACAGTCA 1079
          ||||| |||||| ||| || || |||| |||||||||| |||||
Qy   1017 ATCTCAATAGAAGAGAAAAATTATCGTGTAAATTGACTTTTTCTGAGAGAAGAAGAGG 1076

Db   1080 ACCTCAATAGGAGAGAAAAATGGAACATGTCCGTGTTCTTCAGTGGAGTCAGGAATGAAG 1139
          ||||||||| | ||||||||| | || |||| | ||||| ||| || |||| |||||||
Qy   1077 AAGAGAAGATGCAGG---------AGAAATAGAGATGAAGGAGGAGGAGGAGGAGG 1118

Db   1140 AAGAGAAGAGAGGGCCCGAGAGGAGAGAACTGGGAGGAG 1199
          ||||||||| || ||| ||||||||||| ||||||||||
Qy   1119 ATGCAGTAGTAGAAGAGGCGAGAAATAGTTGCAAATAGCATCTTCAGGGAGGAAGGAGA 1178

Db   1200 AAGCAGTAGGAGTGGAAGGTAGAAAAATGTTCAAACAGAGTTTTTGGATGAAGA 1259
          |||||||| || || |||| |||| ||| |||||| || |||| |||| ||
Qy   1179 GTCTGAGAAAGCTGCAGAGCCCTCTCAGTCTTCCCGGAGTCGCCCCAGAGC 1238

Db   1260 ACCAGAAAAAAGCTTCAGAGCTCTCTCAGGT-------GGACTGCAGGGCTGCCCTGGGG 1312
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Qy   1239 CACTACCTGCTTCCTCTCCAGGAAC 1262

Db   1313 CACTTCCAGTTTCCTCTCCAGAGC 1336
          |||| |||| ||||||||||||||
Qy   1313 CACTTCCAGTTTCCTCTCCAGAGC 1336
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WPI; 2002-673014/72.
DR   P-PSDB; ABG93804.

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                                        GenCore version 5.1.6
                                  Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:           June 14, 2005, 19:51:42 ; Search time 7464 Seconds
                                              (without alignments)
                                              13208.261 Million cell updates/sec

Title:            US-10-775-627A-3
Perfect score:    2590
Sequence:         1 ctcgagattacccttacag...........ctccttttccttcttccctcc 2590

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         34239544 seqs, 1903214700 residues

Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

Database :        EST:*
                  1: gb_est1:*
                  2: gb_est2:*
                  3: gb_htc:*
                  4: gb_est3:*
                  5: gb_est4:*
                  6: gb_est5:*
                  7: gb_est6:*
                  8: gb_gss1:*
                  9: gb_gss2:*

                  Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                    SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	655.8	25.3	741	3	AK052918	AK052918 Mus muscu
2	624	24.1	822	5	BX427830	BX427830
3	610.6	23.6	694	2	BB520266	BB520266
4	565.2	21.8	790	4	BG674823	BG674823
5	529.6	20.4	826	0	CK599151	CK599151 AGENCOURT
6	521.4	20.1	672	2	BB662321	BB662321
7	508.2	19.6	647	7	CV026849	CV026849 4912 Full
8	494.6	19.1	657	7	CR754151	CR754151
9	483.4	18.7	827	5	BU131273	BU131273
10	483.2	18.7	927	7	BU129677	BU129677 603118735
11	480.6	18.6	655	7	CR755417	CR755417
12	457.4	17.7	1077	9	AY411684	AY411684 Homo sapi
13	457	17.7	699	5	BX501677	BX501677 DKFZp779F
14	445.8	17.2	1161	4	BG163322	BG163322 602338256
15	442.4	17.1	1083	9	AY411686	AY411686 Mus muscu
16	441.2	17.0	840	5	BU321841	BU321841 603485910
17	438.6	16.9	991	5	AY411685	AY411685 Pan trogl
18	432.6	16.7	697	5	BU145004	BU145004 603229155
19	422	16.3	983	2	BF205857	BF205857 601868260
20	416.8	16.1	1092	8	BI114696	BI114696 602861723
21	413.2	16.0	1081	2	BF309583	BF309583 601891901
22	409.4	15.8	776	4	BI114212	BI114212 602862572
23	406.8	15.7	506	1	AA840584	AA840584 vw77h09.r
24	404.6	15.6	657	7	CO506878	CO506878 GGEZEB201
25	390.8	15.1	684	7	CO506307	CO506307 GGEZEB101
26	380	14.7	648	7	CO506630	CO506630 GGEZEB101
27	377.6	14.6	812	7	CR439377	CR439377 CR439377
28	376.6	14.5	573	1	AA443443	AA443443 zw94c05.r
29	373.6	14.4	615	4	BJ033623	BJ033623
30	361.2	13.9	751	6	CA342294	CA342294 672134 NC
31	361.2	13.9	775	7	CF290486	CF290486 AGENCOURT
32	361	13.9	945	5	BU537902	BU537902 AGENCOURT
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35	350.6	13.5	800	5	BU220426	BU220426 603756441
36	349.8	13.5	786	7	CF289491	CF289491 AGENCOURT
37	349	13.5	900	5	BU262226	BU262226 603505103
38	348	13.4	1142	5	BU470941	BU470941 603363447
39	347.8	13.4	1455	3	CR677834	CR677834 Tetraodon
40	346.8	13.4	797	7	CK697390	CK697390 ZF101-P00
41	344	13.3	890	5	BU107891	BU107891 603111441
42	342.8	13.2	614	7	CF615149	CF615149 CES008971
43	333.8	12.9	1466	3	CR670382	CR670382 Tetraodon
44	333	12.9	966	5	BU135007	BU135007 603119195
45	332.8	12.8	952	5	BU241018	BU241018 60322733

                                    ALIGNMENTS

```
RESULT 1
AK052918

LOCUS       AK052918                 741 bp    mRNA     linear   HTC 03-APR-2004
DEFINITION  Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
            library, clone:D830041C10 product:hypothetical RING finger/B-box
            zinc finger domain containing protein, full insert sequence.
ACCESSION   AK052918
VERSION     AK052918.1  GI:26343090
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P., and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
```

TITLE   Group Phase I & II Team.
            Analysis of the mouse transcriptome based on functional annotation
JOURNAL   of 60,770 full-length cDNAs
            Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 741)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Miramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /clone="D830041C10"
                     /db_xref="taxon:10090"
                     /tissue_type="heart"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="16 days neonate"
     CDS   151..>741
                     /note="unnamed protein product; hypothetical RING finger
                     B-box zinc finger domain containing protein
                     (InterPro:IPR001841, evidence: InterPro)
                     putative"
                     /codon_start=1
                     /protein_id=1
                     /protein_id="BAC35202.1"
                     /db_xref="GI:26343091"
                     /translation="MSTSLNYKSFSKEQQTMDNLEKQLICPICLEMFTKPVVILPCGH
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                     NIDIYKQESTRPEKKLDQPMCEEHEEERINIYCLNCEVPTCSLCKVFGAHKDCQVAP
                     LTHVFQROKSELSDGIAVLVGSNDRVQGVISQLEDTC"
ORIGIN
Query Match   25.3%; Score 655.8; DB 3; Length 741;
Best Local Similarity   99.7%; Pred. No. 1.1e-161;
Matches 657; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   12 CCCTTACAGAGAGCTGTTCGGGAGCACTCTTCCCTTGGCAGCACACTCAGGGACGCAGGACG 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   83 CACTTACAGAGAGCCCGTTCGGGAGCACCTTTCCCTTGGCAGCACACTCAGGGACGCAGGACG 142

Qy   72 GCAAGGAAATGAGCACTCTTCTCTGAATTACAAGTCTTTTCTCAAAGAGCAGCAGCAATGG 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 GCAAGGAAATGAGCACTCTTCTCTGAATTACAAGTCTTTTCTCAAAGAGCAGCAGACCAATGG 202

Qy   132 ATAACTTGGAAAAAGCAACTGATCTGTCCCATCTGCCTAGACAGTTCACGAAGCCTGTGG 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203 ATAACTTGGAAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGCCTGTGG 262

Qy   192 TCATTCTCCCGTTGCCAGCACAACCTTGTGCAGGACACAACCTGTGCAGGAAATGTGCCAGTGACATCTTCCAGGCCT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   263 TCATTCTCCCGTTGCCAGCACAACCTTGTGCAGGACACAACCTGTGCAGGAAATGTGCCAGTGACATCTTCCAGGCCT 322

Qy   252 CTAACCCGTACTTACCCACACAGAGAGGAGGGCCACCAGCACCGTGGCATCCAGGGGGGCGCCGGCCGCTTCCGGCT 311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323 CTAACCCGTACTTACCCACACAGAGGAGGGCCACCAGCACCGTGGCATCCAGGGGGGCGCCGGCCGCTTCCGGCT 382

Qy   312 GTCCCTCCCTGAGACAATGAGGTGGGTGGTTAGACCAGACAGACAGACAGAGATGCGCAGAGGA 371
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Db   383 GTCCCTCCCTGAGACAATGAGGTGGGTGGTTAGACCAGACAGACAGACAGAGATGCAGAGGA 442

Qy   372 ACCTGCTCGTGGAAAAACATTATTGATTATCTACAAGCAGCAGGCGCCAGAAAAA 431
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Db   443 ACCTGCTCGTGGAAAACATTATTGATTATCTACAAGCAGCAGGCGCCAGAAAAA 502

Qy   432 AAATTGGACCAGCCCATGTGTGAAGAGCATGAAGAGGAACGCATCAACATCTATTGTCTGA 491
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 AAATTGGACCAGCCCATGTGTGAAGAGCATGAAGAGGAACGCATCAACATCTATTGTCTGA 562

Qy   492 ACTGTGAAGTGCCCACCTGTTCCCTGTGTAAGGTTTTTGGGGCCCCATAAGACTGCCAGG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 ACTGTGAAGTGCCCACCTGTTCCCTGTGTAAGGTTTTTGGGGCCCCATAAGACTGCCAGG 622

Qy   552 TGGCTCCCTGACTCATGTGTTCCAGAGCAGAAGTCAGAGACTCAGTGATGGTATTGCTG 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   623 TGGCTCCCCCTGACTCATGTGTTCCAGAGCAGAAGTCAGAGACTCAGTGATGGTATTGCTG 682

Qy   612 TACTTGTGGGGAAGCAACGATAGAAGTCCAGGGTGTGATCAGCCAGCTGGAGGACACCTGT 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   683 TACTTGTGGGGAAGCAACGATAGAAGTCCAGGGTGTGATCAGCCAGCTGGAGGACACCTGT 741

RESULT 2
LOCUS   BX427830   822 bp   mRNA   linear   EST 05-MAY-2004
DEFINITION BX427830 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
            CS0DM012YM10 5-PRIME, mRNA sequence.
ACCESSION   BX427830
VERSION   BX427830.2 GI:47037092
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 822)
AUTHORS   Li,W.B., Gruber,C.; Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30788679.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: Segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 4738.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0AM012BG050QP16c=4738.f.

FEATURES   Location/Qualifiers
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                     /clone="CS0DM012YM10"
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                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL LIVER"
                     /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA

ORIGIN

was primed with a Noti-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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Query Match    24.1%; Score 624; DB 5; Length 822;
Best Local Similarity    85.5%; Pred. No. 3e-153;
Matches  703; Conservative  11; Mismatches 106; Indels  2; Gaps  2;

Qy    245 CAGGGCTCTAACCCGTACTTACTTACCCAACAAGAGGAGGGCCACCGTGGCATCAGGGGGGCCGC 304
          |||||||||||||||| ||| |||| |||||||||||||||||||||||||||||||||||||||
Db      1 CAGGGCCTCTAACCCGTATTTGCCCACAAGAGAGGTACCACCATGGCATCAGGGGGGCCGA 60

Qy    305 TTCCCGTGTCCCTCCTGCAGACATGAGGTGGTGTTTGACAGACATGGGGTCTTATGGACTG 364
          ||||||| ||||||||| ||||||||||||||||||| |||||||||||||||||||||||
Db     61 TTCCGGCTGCCCATCCTGTAGACATGAAGTGGTTTTGGGATGACATGGGGTATATGGACTT 120

Qy    365 CAGAGGAACCTGCTCGGTGGAAAACATTATTGATATATCTACAAGCACAGGAATCCACCAGGCCA 424
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    121 CAGAGGAACCTGCTGGTGGAAAATATCATTGACACTACTACAAGCACAGGAATCCACCAGGCCA 180

Qy    425 GAAAAAAATTGGACCAGCCCCATGTGTGTGAAGAGCATGAAGAGGAACGGCATCAAACATCTAT 484
          ||||| |||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db    181 GAAAAGAAATCCGACCACCAGCCCATGTGGCCAGGAGGGGAACATTGGACCATCAAACATCTAC 240

Qy    485 TGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGTCCAAGGTTTTTTGCGCCCATAAGGAC 544
          ||||||||||| |||||||||||||| ||| |||||||||||||||||| ||||| ||||||
Db    241 TGTCTGAACTGCGAAGTACCCMCCTGTCTCTTGTGTCCAAGGTGTTTTGGTGCACAAAAGAC 300

Qy    545 TGCCAGGTGGCTCCCCTGACTCANTGTTGTTCCAGAGGAGGCAGAAGTCAGAGCTCAGTGATGGT 604
          |||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCCAGGTGGCTCCCTCACTCATGTGTWCCAGAGACAGAAGTCTGAGCTCAGTGATGGC 360

Qy    605 AT-TGCTGTACTTGTGGGAAGCAACGATAGAGTCCAGGGGTGTGATCAGCGACCTGGAGGA 663
          || |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATCCGGCCATCCTCGTGGGCAGCAACGACGATCGAAGTCCAGGAGTGATCAGCCTGGAAGA 420

Qy    664 CACCT-GTAAAAACTATTGAGGAGTGCTGCAGAAAGCAGACAGACCTGTGTGAGAAAT 722
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Db    421 CACCTCGCAAAAACTATCGAGGAGAATGTTGCAGAAAACACAGAGCTTTGTGAGAAGT 480

Qy    723 TTGATCACCTTATACGGCCATACCTCGGAGGGGAAGAAGAAGCAAAGCCATCACTC 782
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Db    481 TTGATTACCTGTATGCGGCATTTTGGAGGGGAAATGAAAATGACCCAAGTCATTACC 540

Qy    783 GAACACGAGGAGGAGAAACTGAACACAGTCCGAACTCTTATCAGGGAAGTATTCCGGATCACC 842
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Db    541 SAACCCWAGGAGGAAAACTGGAACAHTGCCCGTKCCTCGATCAAAAGTAHTCTGATCATT 600

Qy    843 TGGGAACGTATCCAAAGTTCGGTGGACTCAGGAATCCAGTTCATTGATGGAGCCCGGAAATGG 902
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Db    601 TGGGAACGTCTCAAAAGTTGGGTTCAGTTTATGAGCTATGAGAACATTCAGTTCAGTGAGAATGG 660

Qy    903 CAGTATTTCTGCGAATGCCAAGACCCGTTGCAAAGATCGTGGAAGCATCAAAGCGT 962
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Db    661 CAGTGTTTCTGCAGAATGCCAAARRRATCTCCGGAAGCATCAAAAGGCAT 720

Qy    963 TTCAGATGAGAAACTAGAACAAGTTTATGACAACTTCACTGTCAATTCTCA 1022
          ||||||| |||||||||| ||| ||||||||||||||||||||||||||||||
Db    721 TTCAGATGAGGAGAAAAATAGAACATGGCTATAGAACATCACAGTCACAACCTCA 780

Qy   1023 ATAGAGAGAAAGAAAATTATCCGTGAAAATTGACTTTTCTACAGAG 1064
          ||||| ||||:||||||||||||||:|||||||||||||||||||
Db    781 ATAGAGAARAGAATAATACGTGAGGATTGACTTTTACAGAG 822
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LOCUS   BB520266   694 bp   mRNA   linear   EST 25-OCT-2001
DEFINITION BB520266 RIKEN full-length enriched, 16 days neonate heart Mus
            musculus cDNA clone D830041C10 3', mRNA sequence.
ACCESSION   BB520266

prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCGAGGTPAATTAAATTPAATTACCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match   98.1%; Score 610.6; DB 2; Length 694;
Best Local Similarity   98.1%; Pred. No. 9.7e-150;
Matches 628; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

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Qy   31 GGAGCACCTTTCCCTTGGCAGCACACTCAGGGACGCAGGGACGGGAGAAATGAGCACTTC   90
         ||||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Db   57 GGAGCACCTTTTCCCTTGGCAGCACACTCAGGGACGCAGGGACCGCAAGGAAATGAGCACTCT  116

Qy   91 TCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGGACCATGAATAACTTGGAAAAGCAACT  150
         ||||| | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  117 TCTGA--TNACAAGTCTTCTCCAAAGAGCAGCAGGACCATGAATAACTTGGAAAAGCAACT  174

Qy  151 GATCTGTCCCATCTGCCTAGAGATGTTCACGAGAGCCTGTGGTCATTCTCCCTTGCCAGCA  210
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  175 GATCTGTCCCATCTGCCTAGAGATGTTCACGAGAGCCTGTGGTCATTCTCCCTTGCCAGCA  234

Qy  211 CAACCTGTGCAGGAAATGTGCCAGTGACATCTTCAGCCCTCTAACCCGTACTTACCCAC    270
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 CAAACCTGTGCAGGAAATGTGCCAGTGACATCTTCAGCCCTCTAACCCGTACTTACCCAC   294

Qy  271 AAGAGAGGAGCACCACCGTGGCATCAGGGGCCGGCCGCTTCCTGTGTCCCTCTCCTGCAGACATGA  330
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  295 AAGAGAGGAGCACCACCGTGGCATCAGGGGCCGGCCGCTTCCGGTGTCCCTCTCCTGCAGACATGA  354

Qy  331 GGTGGTGTTAGACACAGACAGTGGGTCTTATGGGACTGCTGCAGAGGAACCTGCTTCGTGGAAAACAT  390
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  355 GGTGGTGTTAGACAGACAGTGGGTCTTATGGGACTGCTGCAGAGGAACCTGCTTCGTGGAAAACAT  414

Qy  391 TATTGATATCTTACACAGCAGGAATCCACCAGGCCCAGAAAAAAAATTGGACCACCCCCATGTG  450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  415 TATTGATATCTTACACAGCAGGAATCCACCAGGCCCAGAAAAAAATTGGACCACCCCCATGTG  474

Qy  451 TGAAGAGACATGAAGAGGAAACCGCATCAACATCTATTGTCTGAACTGTGAAGTGCCCCACCTG  510
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  475 TGAAGAGACATGAAGAGGAAACCGCATCAACATCTATTGTCTGAACTGTGAAGTGCCCCACCTG  534

Qy  511 TTCCTTGTGCAAGGGTTTTTTGGGCGGGCCCCATAAGGACTCGCCTCCCCTGACTCACCTG  570
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  535 TTCCTTGTGCAAGGGTTTTTTGGGCGGGCCCCATAAGGACTCGCCTCCCCTGACTCACCTG  594

Qy  571 GTTCCAGAGGGCAGGAAGCTCAGTCAGTGATGGTATTGGCTGCTGTACTTGTGGGBAAGCAACGA  630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  595 GTTCCAGAGGGCAGGAAGCTCAGTCAGTGATGGTATTGGCTGTACTTGTGGGBAAGCAACGA  654

Qy  631 TAGAGTCCAGGGTGTGATCAGCCAGCTGGAGGAGCACCTGT  670
         |||||||||||||||||||||||||||||||||||||||
Db  655 TAGAGTCCAGGGTGTGATCAGCCAGCTGGAGGAGCACCTGT  694
```

RESULT 4

LOCUS   BG674823   790 bp   mRNA   linear   EST 01-MAY-2001
DEFINITION 602620959F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746254 5',
            mRNA sequence.
ACCESSION   BG674823
VERSION   BG674823.1 GI:13906219
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 790)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

FEATURES   Location/Qualifiers
     source   1..790
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4746254"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.5kb. Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Query Match   84.3%; Score 565.2; DB 4; Length 790;
Best Local Similarity   84.3%; Pred. No. 1e-137;
Matches 666; Conservative 0; Mismatches 108; Indels 16; Gaps 2;

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Qy  403 CAAGCAGGAATCCACCAGGCCCAGAAAAAAAAATTGGACCAGCCCATGTGTGAAGAGACATGA  462
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    1 CAAGCAGGAGTCCACCAGGCCCAGAAAAGAAAATCCAGACGCCCCATGTGTGAAGAGACATGA  60

Qy  463 AGAGGAACGCATCAACATCTATTGTCTGAACTGTGAAGTGCCCCACCTGTTCCTTGTGTCCAA  522
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   61 AGAGGAACGCATCAACATCTACTGTCTGAACTGCCGAAGTACCCACCTGCTCTGTTCCGTGCAA  120

Qy  523 GGTTTTTTGGGCGGGCCCCATAAGGACTCGCCTCCCCTGACTCACCTGGTTCCAGGAGCCA  582
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  121 GGTGTTTTGGGCGGGCCCCATAAGGACTCGCCTCCCCTCACTCACTGTGTTCCAGAGCCA  180

Qy  583 GAAGTCAGAGCTCAGTGATCAGTTATTGCTGTACTTGTGGGGAAGCAACGAATAGAGTGTCGG  642
         ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  181 GAAGTCTGAGCTCAGTGATGGATTGCCATGGCCATCGGAGGCAACAAGCAGGAGTCGG  240

Qy  643 TGTGATCAGCCAGCTGGAGGACACCTGTAAAAACTATTGGAAGTGCTGCAGAAAAAGCAGAA  702
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  241 ACAGGACCTGTGTGAGAAATTGATCAACATCTATACCGCATCCTGGAGGAAATGTTGCAGAGAAAACAGAA  300

Qy  703 ACAGGACCTGTGTGAGAAATTTGATCAACACCTGCCAAAACTATGGCATTTTGGAGGGAAGACTGA  762
         ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  301 ACAAGAACTTTGTGAGAAGTTTGATTTACCTGTATGGCATTTTGGAGGAGAAGAATGA  360

Qy  763 AATGACCCAAGCCATCAATTACCCGAACCCAAGAGGAGAAACTGGAACATGTCCGAACTCTTAT  822
         |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  361 AATGACCCAAGTCATTACCCGAACCCAAGAGGAGAAACATGTCCGAACTCTTAT  420

Qy  823 CAGGAAGTATTCCGGATCACCTGGAGAACGTATCCAAGTTGGTGGAGTGGAATCCAGTT  882
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  421 CAAAAAAGTATTCTGATCATTTGGAGAACGTCTCAAAGTTGGTTGGAGTTCAGGGAATTCAGTT  480

Qy  883 CATGGATGAGCCCCGAAATGCCAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAGAT  942
         |||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||
Db  481 TATGGAYGAGCCAGAAATGGCAGTGTTTTCTGCAGAATGCCAAAAACCCTGCTAAAAAAAAT  540

Qy  943 CGTGGAGCATCAAAGGCCGTTTCAGATGGAGGAAACTAGAACAGGTTATGAGATCATGAG  1002
         ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  541 CTCGGAAGCATCAAAGGCATTTCAGGTGGAGGAAACTAGAACAAGGTTATGAGAACATGAA  600

Qy 1003 CCAACTTCACTGTCAATCTCAATAGAGAGAGAGAGAAAGATAATACGTGAAATTGACTTTTCTAG  1062
         |||||||||||| |||||||| |||||||||||||||| ||||||||||||||||||| ||
Db  601 CCACTCACAGTCAACCTCAATAGAGAAGAGAGAGAGAAAGATAATACCGTGAAATTGACTTTACAG  660
```

RESULT 5

```
LOCUS       CK599151                 826 bp    mRNA     linear   EST 22-JAN-2004
DEFINITION  AGENCOURT_17896510 NIH_MGC_234 Rattus norvegicus cDNA clone
            IMAGE:7192411 5', mRNA sequence.
ACCESSION   CK599151
VERSION     CK599151.1  GI:41112287
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE     Unpublished (1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1053 row: a column: 17
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1..826
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7192411"
                     /tissue_type="heart, pooled"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_234"
                     /note="Organ: heart; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from pooled heart tissue from a
                     mix of male and female animals at 8 wk old. Tissues were
                     snap-frozen and kept at -80C for two days before RNA
                     extraction and purification (Tri-reagent method). cDNA was
                     primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCGCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
                     resulted in an average insert size of 2.2 kb. This primary
                     library is normalized (non-normalized primary library is
                     NIH_MGC_233) and was constructed by Express Genomics
                     (Frederick, MD). Note: this is a NIH_MGC library."
ORIGIN
```

```
Query Match             20.4%;  Score 529.6;  DB 7;  Length 826;
Best Local Similarity   93.3%;  Pred. No. 2.8e-128;
Matches  599;  Conservative  0;  Mismatches 34;  Indels  9;  Gaps  4;

Qy  1063 AGAGAGAGGAAGGAAGGAAGAGA-----------TGCAGGAGAAATAGAATGAAGAAGGAG 1109
         |||||||| ||||| ||||||||                 |||||||  |||||||||||
Db   661 AGAGAGATGAAGGATGAAGAAGAGAAGGCGGAGAAGCGAAGAGGAGGAGGAGG         720

Qy  1110 AA---GGAGAGGATGGCAGTAGAAGTAGAAGAAGAAGCAGAGAAAATAGTTCAAATAGCATCTTCAG 1166
         ||   |||||||| || |||||||||| ||||||| |||||||||| |||||||  |||  |||||
Db   721 AAGTGGGAGAGGAGGAGGAGCAGTAGAAGTGGGAGAAGGTAGAAAATGTTCAAACAGAGTTTCCAG   780

Qy  1167 GGGAAGAGGA 1176
         |||||   ||
Db   781 GAGACCGATGA 790

Qy    11 ACCCTTACAGAAGCGTGTTCGGGAGACACCTTTCCCTTGGCAGCACACTCAGGGACGCAGGGAC 70
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RESULT 6

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LOCUS       BB662321                 672 bp    mRNA     linear   EST 26-OCT-2001
DEFINITION  BB662321 RIKEN full-length enriched, 16 days neonate heart Mus
            musculus cDNA clone D830041C10 5', mRNA sequence.
ACCESSION   BB662321
VERSION     BB662321.1  GI:16496076
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
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```
Db    65 ACACTTCCAGAAGCCGTTCGGGAGCAGCACCCTTCCCTTGGGGCCACC-----CAGGGAC 118

Qy    71 GGCAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCAAAGAGCAGCAGCACATG 130
Db   119 GGCTAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCAAAGAGCAGCAGCACATG 178

Qy   131 GATAACTTGGAAAAGGCAGCAACTGATCTCTGTCCCATCTGCCTAGAGATGTTCACGGAAG 190
Db   179 GATAACTTAGAAAAAGGCAACTGATCTCTGTCCCATCTGCCTAGAGATGTTCACCAAGCCG 238

Qy   191 GTCATTCTTCCCTTGCCAGCACAAACCTGTGCAGGAAATGTGCCAGTGACATCTTCCAGGC 250
Db   239 GTCATTCTTCCCGTTGCCAGCATAAACCTGTGCAGGAAGTGCCCAGTGACATCTTCCAGGCC 298

Qy   251 TCTAACCCGTACTTACCCACAAAGAGAGGAGCCACCACCGTGCCATCAGGGGCGCCCTTCGC 310
Db   299 TCTAACCCGTACTTACCCACAAAGAGGAGCACCACCGTGCCGTCGGGGCCGCTTCCGC 358

Qy   311 TGTCCCTCCTTCGACATGAGGTGGTTAGACAGAGGCATGAACAGTGGGGTCTTATGGAGAGG 370
Db   359 TGTCCCTCCTTCGACAGCAGATGAGGTGGTTAGACAGAGGCATGGGTCTTATGGAGAGG 418

Qy   371 AACCTGCTCGTGGAAAACATTATTGATATCTACAGACAGGAATCCACCAGGCCAGGAAAA 430
Db   419 AACCTCCTTGTCGAGGAACATCATTGATATCTACAGACAGGAAATCCACCAGGCCAGGAAAA 478

Qy   431 AAAATGGACCAGCCCATGTGTTGGAGGAGCATGAAGAGGAAGCCATCAACACATCTATTGT 490
Db   479 AAGTTGGACCAGCCCATGTGTGAGGAGCATGAAGAGGAACCCATCAACACATCTACTGTCTG 538

Qy   491 AACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCCATAAGGACTGCCAG 550
Db   539 AACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGTCGTCATGATGGTGATTGCT 598

Qy   551 GTGGCTCCCCTGACTCATGTGTTCCAGAGGGCAGAGCTCAGTGATGATGTGATTGCT 610
Db   599 GTGGCTCCCCTGACCCCATGTGTTCCAGAGGGGCAGAAGTCAGAGCTCAGTGAT-GTATTGCT 657

Qy   611 GTACTTGTGGGGAAGCAACGATTAGAGTCCAGGGTGTGATCAGC 652
Db   658 GTACTTGTGGGGAAGC-ACGACAGAGT-CAGGGTGTGATCAGC 697
```

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES   Location/Qualifiers
  source   1..672
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="DB3004IC10"
                     /tissue_type="heart"
                     /dev_stage="16 days neonate"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 16 days neonate
                     heart"
                     /note="Site 1: SalI; Site 2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCGGCCAACTCGAGTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCGGATTAATTAATCCCCCCCCCCCCCC 3'], cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN
Query Match   20.1%;   Score 521.4;   DB 2;   Length 672;
Best Local Similarity 98.2%;   Pred. No. 3.8e-126;
Matches 558;   Conservative   0;   Mismatches   7;   Indels   3;   Gaps   3;

Qy   12 CCCTTACAGGAAGCTGTTCGGGAGGCACACTCAGGGACAGGGACG 71
           ||||||||||||||||| |||||||||||||||||||||||||||
Db   83 CACTTACAGGAAGCCGTTCGGGAGCACCTTTCCCTTGGCAGGCAACTCAGGGACACACGGGACG 142

Qy   72 GCAAGGAAAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCAAAAGAGCAGAGGACCATGG 131
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 GCAAGGAAAATGAGCACTTCTCTGAATTACAAGTCTTTTCTCCAAAAGAGCAGAGGACCATGG 202

Qy   132 ATAACTTGGAAAAGCAACTGATCTGTTCCCATCTGCCTTAGACGATGTTCACGGAAGCCTGTGG 191
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   203 ATAACTTGGAAAAGCAACTGATCTGTCCCCATCTGCCTTAGACGATGTTCACGGAAGCCTGTGG 262

Qy   192 TCATTCTCCCTTGCCCAGCAACCTGTGCCAGGAAAATGTGCCAGTGACATCTTCCAGGCCT 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   263 TCATTCTCCCTTGCCCAGCAACCTGTGCCAGGAAAATGTGCCAGTGACATCTTCCAGGCCT 322

RESULT 7
CV026849
LOCUS   CV026849   647 bp   mRNA   linear   EST 20-AUG-2004
DEFINITION   CV026849 4912 Full Length cDNA from the Mammalian Gene Collection Homo
               sapiens cDNA 5' similar to BC007750, mRNA sequence.
ACCESSION   CV026849
VERSION   CV026849.1   GI:51484871
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 647)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
               Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
               Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
               Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
               Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE   Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT   Contact: Vidal M
               Marc Vidal Laboratory
               Dana Farber Cancer Institute
               1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
               Tel: 617 632 5180
               Fax: 617 632 5739
               Email: Marc.Vidal@dfci.harvard.edu
               ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
               results from a PCR reaction using an MGC full-length cDNA as
               template DNA and ORF specific primers
               PCR Primers
               FORWARD: ATGAGCGGCATCTCTGAATTAC
               BACKWARD: CATTCATTTAGGGAGGTTCAACCA
               Insert Length: 647   Std Error: 38.00
               Plate: 11063   row: 01   column: H
               Seq primer: ACTGGCGTTCGTTTACAACGTGACTGGGAAAAC
               High quality sequence start: 101
               High quality sequence stop: 646
               POLYA=No.

FEATURES   Location/Qualifiers
  source   1..647
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="mixed"
                     /clone_lib="Full Length cDNA from the Mammalian Gene
                     Collection"

Qy   252 CTAACCCGTACTTACCCACAAGAGGAGGAGGCACCACCGTGGCATCAGGGGGCGCGCTTCGGCT 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323 CTAACCCGTACTTACCCACAAGAGGAGGAGGCACCACCGTGGCATCAGGGGGCGCGCTTCGGCT 382

Qy   312 GTCCCTCCTCGCGACCATGAGGTGGTGTTAGACAGAGACAGCATGGGGGTCTCATGGACTGCAGGAGGA 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   383 GTCCCTCCTCGCGACCATGAGGTGGTGTTAGACAGAGACAGCATGGGGGTCTCATGGACTGCAGGA 442

Qy   372 ACCTGCTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAGGCCAGAGAAAA 431
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   443 ACCTGCTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAGGCCAGAGAAAA 502

Qy   432 AATTGGACCAGCCCATGTGAAGAGCCATGAAGAGCATCAACATCTATTGTCTGA 491
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 AATTGGACCAGCCCATGTGAAGAGCCATGAAGAGCATCAACATCTATTGTCTGA 562

Qy   492 ACTGTGAAGTGCCCCACCTGTTCCTTGTCTGCAAGGTTTTTGGCGCCCCATAAGGACTGCCAGG 551
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   503 ACTGTGAAGTGCCCCACCTGTTCCTTGTCTGCAAGGTTTTTGGCGCCCCATAAGGACTGCCAGG 562

Qy   552 TGGCTCCCCTGACTCANGTGNTTCAGAAG 579
           ||||||||| ||||| ||| |||||||
Db   563 ACTGTGAAGTG-CCACCTGTTCCTTGTCTGCAAGGTTNNTGGGCGCCC-TAAAGACTGCCAGG 620

Qy   621 TGGCTCCCC-GACTCANGTGTTCAGAAG 647
           ||||||||| |||| ||||||||||
Db   621 TGGCTCCCC-GACTCANGTGTTCAGAAG 647

RESULT 8

```
REFERENCE    1  (bases 1 to 657)
AUTHORS      Cros,N., Tkatchenko,A.V., Pisani,D.F., Leclerc,L., Leger,J.J.,
             Rattus.
ORGANISM     Rattus norvegicus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
SOURCE       Rattus norvegicus (Norway rat)
KEYWORDS     EST.
VERSION      CR754151.1  GI:51866108
ACCESSION    CR754151
             cDNA clone GP0AAA11ZD06, mRNA sequence.
DEFINITION   CR754151 Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus
LOCUS        CR754151                 657 bp    mRNA    linear  EST 02-SEP-2004
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ORIGIN

```
Qy         Query Match    19.6%;  Score 508.2;  DB 7;  Length 647;
           Best Local Similarity  89.0%;  Pred. No. 1.2e-122;
           Matches  549;  Conservative  0;  Mismatches  68;  Indels  0;  Gaps  0;

Qy       80 ATGAGGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGCCATGGATAACTTG 139
            |||| ||| ||  |||||||  ||||| ||||||||||||||||||||| |||||| |||
Db        1 ATGAGGCGCATCCTTCTGAATTACAAATCTTTTTTCCAAAGAGCAGCAGACCATGGATAACTTA 60

Qy      140 GAAAAGCAACTGATCTGTGTCCCATCTCGCTTAGAGATGATGTTCACGGAGAGCCTGTGGGTCATTCTC 199
            ||||||||||||||  ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       61 GAGAAGCAACTCATCTGTGTCCCATCTCGCTTAGAGATGTTCACGGAGAGCCTGTGGGTTGATTCTC 120

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Qy      500 GTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGGCCCATAAGGACTGCCAGGTGGCTCCC 559
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Db      421 GTACCCACCTGTTCGTCCTCTGTGCAAGGTGTTTGGTGGCACAAAGACTGCCAGGTGGCTCCC 480

Qy      560 CTGACTCAGTGTGTTCCAGAGGCAGAAGTCAGAGAGCTCAGTGTATTCGTCTGTACTTGTG 619
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Qy      620 GGAGCAACGATAGAGTCCAGGGGTGTGATCAGCTGGAGGCAGACCTGTAAAACTATT 679
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Qy      680 GAGGAGTGCTGCAGAA 696
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Db      601 GAGGAAGTTGCAGAA 617
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RESULT 9

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Db   530 CTAACTTGTTGAGAAAATGATTATGTCTCAGAACAAAAAAATTACAGAAAATACTCTGATGAA  589

Qy  1944 GAAACTTGATCTTCTGCAAAACTTTCATTTGTGTGAGAAAACCTTCTGAAGGTTGTGTGTAGG  2003
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DEFINITION 603116770F1 CSEQCHL21 Gallus gallus cDNA clone ChEST72k17 5', mRNA
            sequence.
ACCESSION   BU131273
VERSION   BU131273.1   GI:25343198
KEYWORDS   EST.
SOURCE   Gallus gallus (chicken)
  ORGANISM Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 827)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE   A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT   Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 0161208930
            Fax: 0161236049
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES   Location/Qualifiers
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                     uni-directionally cloned cDNA libraries from messenger RNA
                     for improved 3' end DNA sequencing by Glenn Fu, et al.
                     U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
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ORIGIN

Query Match   18.7%;   Score 483.4; DB 5; Length 827;
Best Local Similarity   77.2%;   Pred. No. 4.6e-116;
Matches 626; Conservative   0; Mismatches 181; Indels   4; Gaps 3;

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Db     3 CGGTGGTCATCCTGCCCGCAGCATAACCTCTGCAGGAAAATGCGCCAGTGATGATATTTCC  62
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Qy   246 AGGCCTCTAACCCGTACTTACCCACCACAAAGAGGAGGAGGCACCACCGTGGGCCATCAGGGCCGCT  305
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Qy   306 TCCGCGTGTCCCTCCTCGCGCAGACATGAGGTGGTGGTGTTAGACACATGGGGGGTCTATGGAACTGC  365
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Qy   426 AAAAAAAAATTGGACCAGCCCCAGTGTGGAAGAGCATGAAGAGGAAGCGCATCAACATCTATT  485
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Qy   786 CACAGGGAGGAGAAACTGGAACATGGGAGAGGTATTATGA  825
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Qy   846 AGAAACCTATCCAAGTTGGGTGGAGTCAGGAATCCAGTTCATCATGG  892
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Qy   904 AGTATTTCTGCGAGAATGCCAAGAC-CCTGTTGCAAAGATCGTGGAGGCCATCAAAGGCGT  962
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RESULT 10

LOCUS   BU129677   927 bp   mRNA   linear   EST 25-NOV-2002
DEFINITION 603118735F1 CSEQCHL21 Gallus gallus cDNA clone ChEST77e9 5', mRNA
            sequence.
ACCESSION   BU129677
VERSION   BU129677.1   GI:25341494
KEYWORDS   EST.
SOURCE   Gallus gallus (chicken)
  ORGANISM Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 927)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE   A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: June 14, 2005, 16:30:06 ; Search time 10746 Seconds
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Post-processing: Minimum Match 0%
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                 12: gb_sy:*
                 13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1261	48.7	2098	6	AK091728	AK091728 Homo sapi
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ALIGNMENTS

RESULT 1
AX418850

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DEFINITION  Sequence 3 from Patent WO0206318.
ACCESSION   AX418850
VERSION     AX418850.1  GI:21523714
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Olson,E.N. and Spencer,J.A.
  TITLE     Methods and compositions for stabilizing microtubules and
            intermediate filaments in striated muscle cells
  JOURNAL   Patent: WO 0206318-A 3 24-JAN-2002;
            BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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ORIGIN
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Matches 2590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  1261 ACCGTTTTCATCCATGCCACCTGCTGCAGATGTCCTGGTGTCCAGTGACAGGGGGTGCC 1320
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Db  1261 ACCGTTTTCATCCATGCCACCTGCTGCAGATGTCCTGGTGTCCAGTGACAGGGGGTGCC 1320

Qy  1321 CATTGGCTCTCACGACACCACACGTCTGAAACTTCAGCGAGCCCTTCAGCGACGGGGAAACTGC 1380
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Qy  1381 GGATCCCTTGTTTTTACCCTAGTTGTTGTATAAAGGCCAAAGCCGGAAAACCCC 1440
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Qy  1501 CAGTGTGCAGTCCGCAGAAGTGGCAGAGCGCAACAATGAGCAGCAGCGGAGTGG 1560
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Qy  1681 TTCTCCTTCTCCTGGTTTGAATTCCCTAAAATGAATAATAATATTATTCGTTGCTGCCCC 1740
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Qy  1741 TGTCTCGCCTGGCTGAAAAGCACATAGGCAGGAAACAGGTGGAAATTCACCACCGATTC 1800
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Qy  1801 ATATGAAGGGGACCTTGGACAGGATTTCTGAAAGGCAAACAAACAATACAACACCACC 1860
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Qy  1861 ACCCTTTAATTCCAGATGACTTATCTCACTCATTGAGAAATGATTATGTCCAGAACAAA 1920
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Qy  1921 ATTACAGAAAAATACTCTTCTGAAGAAAACTTGATCTTTCTGCAAAATCTTTCATTTGTGTGAG 1980
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Db  1921 ATTACAGAAAAATACTCTTCTGAAGAAAACTTGATCTTTCTGCAAAATCTTTCATTTGTGTGAG 1980

Qy  1981 AAACCTTCTGAAAGGTTGTGTAGGTGTGGGTCATGCCTGTTATCAGCCATAAGTGCCAAG 2040
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Db  1981 AAACCTTCTGAAAGGTTGTGTAGGTGTGGGTCATGCCTGTTATCAGCCATAAGTGCCAAG 2040

Qy  2041 TGGTAACAAACTGGCAGAAGTGGGCAGAAACACTCTCCCAGCCTTCAGGCTTCTGGTTATTTTAGGAC 2100
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Qy  2101 GCTTGTGCCTTTTGCTTTTTCTCCCTTAGCATTGCAGGTGGTGATGTTCAGTGTCAGT 2160
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Qy  2161 TCCAAACTGACCGATTTATCAAAATATGGAGAGATTGGTCACTGACCAAAGCTATGTGAGGGC 2220
Db  2101
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Db  2161 TCCAAACTGACCGATTTATCAAAATATGGAGAATTGGTCACTGACCAAAGCTATGTAGGGC
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Qy  2341 TCTAACCTTATTTACATATCTCATAATCATATCATGTATTAGGSCATTTTAATTGAATTT 2400
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Qy  2401 CAAAGAGGAGCTGTCTACTTTTTCTTTCTTTCTTTTTAAGTGTCTCCTCCGCAGCAATCTGTATAATCTGTG 2460
Db  2401 CAAAGAGGAGCTGTCTACTTTTTCTTTCTTTCTTTTTAAGTGTCTCCTCCGCAGCAATCTGTATAATCTGTG 2460
Qy  2461 GAGCAAACTGCATGGATTTAAGTATACACAACAATTCTCCCCCTTCCCCCTTCTCTCCTCTC 2520
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Qy  2581 TTCTTCCCTCC 2590
Db  2581 TTCTTCCCTCC 2590
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LOCUS       HSA291712              2202 bp    mRNA    linear   PRI 06-JUL-2001
DEFINITION  Homo sapiens mRNA for RNF29 gene for ring finger protein 29.
ACCESSION   AJ291712
VERSION     AJ291712.1  GI:13160384
KEYWORDS    ring finger protein 29; RNF29 gene.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Centner,T., Yano,J., Kimura,E., McElhinny,A.S., Pelin,K.,
            Witt,C.C., Bang,M.L., Trombitas,K., Granzier,H., Gregorio,C.C.,
            Sorimachi,H. and Labeit,S.
TITLE       Identification of muscle specific ring finger proteins as potential
            regulators of the titin kinase domain
JOURNAL     J. Mol. Biol. 306 (4), 717-726 (2001)
MEDLINE     21140140
PUBMED      11243782
REFERENCE   2  (bases 1 to 2202)
AUTHORS     Centner,T.
TITLE       Direct Submission
JOURNAL     Submitted (12-FEB-2001) Centner T., Structure and Biocomputing,
            EMBL-Heidelberg, Meyerhofstrasse 1, Heidelberg 69112, Germany
REMARK      Revised by author 22-FEB-2001
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                     AILVGSNDRVQGVISLQEDTCKTIEECCRKQOELCEKFDYLGILEERKNEMTQVIT
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ORIGIN
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Query Match             50.5%;  Score 1309.2;  DB 9;  Length 2202;
Best Local Similarity   80.2%;  Pred. No. 0;
Matches 1689; Conservative   0; Mismatches 368; Indels  49; Gaps  11;

Qy   66 GGGACGGCAAGGAAAATGAGCACTTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGA 125
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Db  119 GGGACAGCGAGGAGAGATGAGCCGCATCTCTGAATTACAAATCTTTTTCCAAAGAGCAGCAGA 178
Qy  126 CCATGGATAACTTGGAAAAGCAACAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGC 185
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Qy  186 CTGTGGTCATTCTCCCTTGCCAGCACAACCTGTCCAGAGAAATGTGCCCAGTGACATCTTCC 245
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Db  239 CTGTGGTGATTCTCCCTTGTCAGCAACCTGTGTAGGAAATGTGCCCAGTGATATTTTCC 298
Qy  246 AGGGCCTCTAACCCGTACTTACCCACAAGAGGAGGCACCACCGTTGGCCATCAGGGGCCGCT 305
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Db  299 AGGGCCTCTAACCCGTATTTGCCCACAAGAGGAGGCGCCACCGTTGGCCATCAGGGGGCCGAT 358
Qy  306 TCCGCTGTCCCTCCTGCGCAGACATGAGGTGGTGTTGACAGAGCATGGGGGTCTTATGGACTGC 365
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Db  359 TCCGCTGCCCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTC 418
Qy  366 AGAGGAACCTGCTCTGGTGGGAAAACATTATTGATATATCTACAAGACAGCAGGAAATCCACCAGGCCAG 425
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Db  419 AGAGGAACCTGCTGTGGTGGGAAAATACATTTACAATGCTACAAGACAGCAGGAGTCCACCAGGCCAG 478
Qy  426 AAAAAAAAAATTGGACACAGCCCATGTGTAGAAGCATGAAGGACAACAACATCTATT 485
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Qy  486 GTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTGGGCGCCCATAAGGACT 545
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Db  539 GTCTGAACTCGGAACGTACCCCACCTGCTCTCTGTGCAAGGTGTTTGGTGCACACAAAGACT 598
Qy  546 GCCAGGTGGCTCCCCTGACTCATGTGTTTCCAGGAGCAGCAGAAGTCAGAGCTCAGTGATGGGTA 605
         |||||||||| |||| ||||||||||||||||||||| |||||||||||||||||||||
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Qy    606 TTGCTCTTACTTGTGTGGGAAGCAAACGAGATAGAGTTCCAGGGTGTGATCACAGCCAGCTTGGGAGGACA 665
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Db    659 TCGGCCAATCTTCCTCCTTTTCCTGG-TTGAACTCCCTAAATGAATGATATTCATTCCAA 718

Qy    666 CCTGTAAAACTTATTGAGAGTGCTCGCAACGATCGAGTTGATCAGCCAGCTGGAAGACA 725
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RESULT 3

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AX747148
LOCUS           AX747148               1925 bp    mRNA            linear   PAT 20-JUN-2003
DEFINITION      Sequence 673 from Patent EP1308459.
ACCESSION       AX747148
VERSION         AX747148.1  GI:32131536
KEYWORDS
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS     Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
              Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
              Tanechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
              Masuho,Y.
  TITLE       Full-length cDNA sequences
  JOURNAL     Patent: EP 1308459-A 673 07-MAY-2003;
              Helix Research Institute (JP) ; Research Association for
              Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1..1925
                     /organism="Homo sapiens"
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ORIGIN

Query Match             48.9%;  Score 1266.4;  DB 6;  Length 1925;
Best Local Similarity   82.0%;  Pred. No. 1.1e-309;
Matches 1571;  Conservative    0;  Mismatches 301;  Indels  44;  Gaps   8;
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Db    93  CCATGGGATAAACTTAGAGAAGCAACTCATCTGTCCATCTGCTTAGAGAGATGTTCACGAAAC  152

Qy   186  CTGTTGGTCATTCTCCCTTGCCAGCAGCAACCTGTCGCAGGAAAGTTGCCAGTGACATCTTCC  245
Db   153  CTGTGGGTGATTCTCCCTTGTCAGCAGCAACCTGTAGGGAAATGTTGCCAGTGATAATTTCC   212

Qy   246  AGGGCCTCTAACCCGTACTTACCCACAAGAGAGGGGCCGGCT                        305
Db   213  AGGGCCTCTAACCCGTATTTCCCACAAGAGAGGGGCCGAT                          272

Qy   306  TCCGCTGTCCTCCTGCAGACATGAGGGTGTTAGACAGACTGGGGTCTATGGACTGC          365
Db   273  TCCCCTGCCCATCCTGTAGACATGAAAGTGGTTTTGGATAGACATGGGGTATATGGACTTC    332

Qy   366  AGAGGAACCTGCTCGTTGGTGGAAAACATTATTGATATATCAACGCAGGAAATCCACCAGCCAG  425
Db   333  AGAGGAACCTGCTCGTTGGTGGAAAATATCATTGACATTAACAAGCAGGAGTCCACCAGGCAG  392

Qy   426  AAAAAAAATTGGACAGCACCCCATGTTGTTGAAGCACATGAAGACGGCACATCTACTTATT    485
Db   393  AAAAGAAAATCCAGACCAGCCCTATGTTGCGGAGGAAACATGAAGAGGGCATCAACATCTACT  452

Qy   486  GTCTGAACTGTGAAGTGCCCACCCTGTTCCTTGTGGCAAGGTTTTTGGGCCCCATAAGGACT   545
Db   453  GTCTGAACTGCGAAGTACCCACCACCTGCTCTCTGTCCAAGGTGTTTTGGGTGCACAAAGACT  512

Qy   546  GCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGGCAGAAGCTCAGTGGGTA            605
Db   513  GCCAGGTGGCTCCCCCTCACTCACGTGTTCCAGAGGGCAGAAGGTCTCAGTGATGGCA       572

Qy   606  TTGCTGTACTTGTGGGAACAACGATAGAGTCCCAGGCGGTTGATGCCAGCTGAGGACA        665
Db   573  TCGCCGCCATCCTTGCGTGGGCAGCGAACGATCAGCGAGCTGGAAGACA                632

Qy   666  CCTGTAAAACTATTGAAGGGGAGTGCTGCTGCAGAAAGGCAGAGAAGGACCTGTGTGAGAAATTTG  725
Db   633  CCTCCAAAAACTATCGAGAATGTTGCAGAAAAACAAGACCTTTGTGAGAAGTTTG          692

Qy   726  ATCACCTATACGGCATCCTGAGGAGGAGAAGACTGAAAATGACCCAGCCCATCACTCGGAA    785
Db   693  ATTACCTGTATGGCATTTTGGGAGGAGAGAATGACACCCAAGTGTCATTACCCGAA         752

Qy   786  CACAGGAGGAGAAACTGGAACATTGGAACACTCTTATCAGGAGTGTATTCATCACCTGG       845
Db   753  CCCAAGAGGAGGAGAAACTGGAACATGGTCCGTGCCTCTCGATCAAAAAGTATTCTGATCATTTGG  812

Qy   846  AGAACGGTATCCAAGTTGGTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAATGGCAG  905
Db   813  AGAACGTCTCAAAGTTGGTTGGTCAGGAATTCAGTTTATGGATGAGCCCAGAAATGGCAG     872

Qy   906  TATTTCTGCAGAATGCCAAGACACCCTGTTGCAAAAAGATCGTGGGACAGCATCAAAAGCGTTTC  965
Db   873  TGTTTCTGCAGAATGCCAAAACCCCGGACATCAGAAAATCTCGGACAGCATCAAAAAGGCATTTC  932

Qy   966  AGATGGCAGGAAACTAGAGAACAAGGTTATGAGAACATCATGAGCAACTTCACTCTGTCAATCTCAATA  1025
Db   933  AGATGGCAGGAAACTAGAAGAACACTTCACACTGTCAACTTCAATA                    992

Qy  1026  GAGAAGAAAAAAATTATCCGTGAAAATTGACTTTTTCTTAGAGAAGAAGAGGAAGAGATG      1085
Db   993  GAGAAGAAAAAGAAAAGATAATTAACGTGAAAATTGACTTTGACTGAGAAGATGAAGAAAGAG   1052

Qy  1086  CAGGAGAAATAGATGAAGAAGGAGAAGGAGACA                                1130
Db  1053  AAGAAGAGGCGGAGAGAAAAATAGGAGAGAAAGGAGGAGAAGTGGGAGAGAGCAGTTAGAAG------GGATGCAGTAGAAG  1112

Qy  1131  TAGAAGAGGCGAGAAAAATGTTCAAATAGCATCTTCAGGGAGAGAGAGTCTGAGGAAG       1190
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Qy  1191  CTGCGAGAGCCCCTCTCAGCTTCAGGTCGGCCCCCAGAGCCCACTACCTGCTT            1250
Db  1173  CTTCAGAGCTCTCCAG------CTGGAGCTGCAGGCTGCCCGGGGCCACTTCCAGTTT        1226

Qy  1251  CCTCTCCAGAACCGTGTTTCATCCATTGCACCACTGCTGCTTCAGATGTCCAGCAGGGGG     1310
Db  1227  CCTCTCCAGAGCCACCTCCACCCTGCCACCTTGCTGCGGGATGCCCCTGTGACACAGGGGG    1286

Qy  1311  AGGTGGTGCCCATTGCTCTCGACAGCACAGCACACAGTCTGAAACTTCAGGCGCAG         1370
Db  1287  AGGTTGTACCCACTGGCTTCGAGACGACCACAGAGTCTGAAAACTCCAGTCCTGCAGCAG      1346

Qy  1371  CGGAAACTGCGGATCCCTGTTTTTTACCCTAGTTGTATTAAAGGGCAAAAGAACCA         1430
Db  1347  CAGAAACTGCGGAATCCCCTTGTTTTTTACCCTAGTGCACCTGTTATAAAGGGCCAAAACCGGAAAGCCA  1406

Qy  1431  GCTCCAACCCCACCTTGCACTCATGGGAGGTGAAAGGTTCAAATAGGGCCTTCGGGGCA      1490
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Qy  1491  TTGAGGATTCCAGTGTGCAGTCCGCAGAAGTGGCAGAGGCCAACCAATGAGCAGGCAG       1550
Db  1467  CTGAGGATTCGAAATGTGACGGAAGGTGGCGCGCAGAGGTTGGAGAGAGGGCAG            1526

Qy  1551  CAGTGAGTGGTAAAGGAGTGTCTAGTTGAACCTCAGCTACCCTCTCAGAATTGGAGGGCCC    1610
Db  1527  CTGTGAGTGGTGAAGGAAACTAGTGCACCTGGCCACCTGCTACTTCTCAGATTTGAAGGGCTC  1586

Qy  1611  CTTCTCTCCCCAGGGGACCAGTCTGCAGCCCTTGGGAGTGGGGGG--GGTGGATCCTGAGCCAG  1669
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Qy  1670  CTCGCCACAGTCTTCTCCTCCCTCGGTTTGAAATTCCAGATGACTTATCCTAC--TCATTGGAAAATGA  1729
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Qy  1730  TTGCTGCCCCC--CTGTCTCGCTCGGCTCGGTGAAAAGCACATAGGCAGAAAACAGGGTGAAAT  1788
Db  1647  CTGGCCATATCTTCTTCTCTTTCCTAAAATGAATGACTTATCTTGGGGGAGAAAGA          1705

Qy  1789  TCACCACGATTCA---TATGAAAGGGGGACCTTCTGGACAGCAGGATTTCTGAAAGGCAAAACAAAA  1845
Db  1706  CTGCTGCCCCTCTGTCTCGCTGGCTCGGCAGGCAGCAGCAAGTGAA                    1765

Qy  1846  CAATCAACAACACCACCCCTTTAATTCCAGATGACTTATCTCAC--TCATTGAGAAAATGA     1904
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Qy  1905  TTATGCTCGAACAAAAATACAGAAAAATACTCTTCTGAGAGAAACTTGATCTTCTGC        1960
Db  1814  ------AAAATAGCCCCAAAACTGCAAATTCCATATGACTTATCTTAACATCTTGGGGGAAAGA  1869

Db  1870  ATATTTTGAGAAAAATAGTTGCCAGAGAAAGCACTGGAAATAATAAACTTGATCTTTATAC    1925
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RESULT 4
AK091728
LOCUS   AK091728   1925 bp   mRNA   linear   PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ34409 fis, clone HEART2001931, moderately
            similar to Mus musculus RING-finger protein MURF mRNA.
ACCESSION   AK091728
VERSION   AK091728.1 GI:21750167
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
            Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
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            Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,
            Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
            Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,

REFERENCE   2
  AUTHORS   Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,
             Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,
             Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
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             Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
    TITLE   Complete sequencing and characterization of 21,243 full-length
             human cDNAs
  JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
   PUBMED   14702039
REFERENCE   3 (bases 1 to 1925)
  AUTHORS   Isogai,T. and Yamamoto,J.
    TITLE   Direct Submission
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 1925)
  AUTHORS   Isogai,T. and Yamamoto,J.
    TITLE   Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
             Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
             (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
  COMMENT   NEDO human cDNA sequencing project supported by Ministry of
             Economy, Trade and Industry of Japan; cDNA full insert sequencing:
             Research Association for Biotechnology (RAB); (cDNA library
             construction: Helix Research Institute (HRI) (supported by Japan
             Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
             HRI, and Biotechnology Center, National Institute of Technology and
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ACCESSION   AJ243489
VERSION     AJ243489.1  GI:14588847
KEYWORDS    alternative splicing; MURF2; RING finger protein 29; RNF29 gene;
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REFERENCE   1
  AUTHORS   Iakovenko,A. and Gautel,M.
  TITLE     Titin-associated zinc-finger proteins link titin kinase to
            transcriptional control
  JOURNAL   J. Muscle Res. Cell Motil. 21, 833-833 (2000)
REFERENCE   2
  AUTHORS   Pizon,V., Iakovenko,A., Van Der Ven,P.F., Kelly,R., Fatu,C.,
            Furst,D.O., Karsenti,E. and Gautel,M.
  TITLE     Transient association of titin and myosin with microtubules in
            nascent myofibrils directed by the MURF2 RING-finger protein
  JOURNAL   J. Cell. Sci. 115 (Pt 23), 4469-4482 (2002)
  MEDLINE   22302063
   PUBMED   12414993
REFERENCE   3  (bases 1 to 2098)
  AUTHORS   Gautel,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie,
            Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse
            11, Dortmund, 44227, GERMANY
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Qy   1491 TTGAGGATTCCAGTGTTGCAGTGTCCGCGAGAGAAGTGGCCGAAGCCGCAACCAATGAGCAGGCAG 1550
          |||||| |||||| ||||||||| |||||||||  || |||||| ||||||||||||||||||
Db   1647 CTGAGAGATTCGAAATGTTACGGGAAGGCAGAAGTCGCAGCGCCTCAGCTACCTCTCAGATTGGCAG 1706

Qy   1551 CAGTGAGTGGTGTAAGGAGGTCTAGTTCAACTGCAGCTACCTGCGAGCTACTTCTCGATTGGATTGAGGGCTC 1610
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Db   1707 CTGTGAGTGGGTTAAGGAAGAAACTAGTGCACCTGCAGCTACTTCTCTCGATATGGATTGAGGGCTC 1766
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Qy   1611 CTTCTCCCCAGGGACAGTCTCCAGCGCCTTGGGGGAGTGGGGGTGG-GGTGGTCCTGACCCAG 1669
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Db   1767 CTCCCCCTTCCAGGGACAGGCTGCCAGCTCAGCAGCCAGCGGGGCAGTGGGAGGCTCAGTGATGGCCAG 1826

Qy   1670 CTCGGCCACGTCGTCCTTCCTTTCTCCGTGTTTGAATTCCCTAAATGAATAATATTATTCTCG 1729
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Db   1827 CTCGGCCACTATCTTCTCTCTTTCCTTTTCCCTGG-TTGAACTCCCTAAAATGAATGAATATTCATTCCAA 1885

Qy   1730 TTGCTCGCCCC-CTGTCTGCCCTGGGTCTGAAAAAGGCACATAGGCGCAGCAGGAAACAGGGTGGAAAT 1788
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Db   1886 CTGCTCGCCCCTTGTCTGCCCTGGGTCTGAGATGCATGTGGGCAGCAGGAAACAGGGTGAAA 1945

Qy   1789 TCACCACGATTCA---TATGAAGGGGACCCTCTGGACAGGAGATTTCTGAAAAAGCAAAA 1845
          ||||||||||||    ||||||||||||||||||||| ||||||||||||||||||||||
Db   1946 TTAATATTATGCAGATGATGAAGAGGGACCCTCTGAACAGGAGATTTCTGAAAAAGCAAAA 1993

Qy   1846 CAATACAACACCACCACCCTTTAATTCCAGATGACTTATCTCAC--TCATTGAGAAATGA 1904
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Db   1994 ----AAAATAGCCCCAAACTGCAAATTCCATATGACTTATCTAACACATCTTGGGGGAGAAAGA 2049

Qy   1905 TTATGCTCAGAACAAAAATACAGAAAATATACTTCTGAAAGAAACTTGAT 1953
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Db   2050 ATATTTTGAGAAAAATAGTTGCAGAAAGCACTGGAAAAATAATAAACTTGAT 2098
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RESULT 6

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              LHVFQRQKSELSDGIAILVGSNDRVQQVISQLEDTCKTIEECCRKQOELCEKFDYL
              YGILEERKNEMMTQVVITRTQEEKLEHVRALIKKYSDHLENVSKLVESGIQFMDEPEMAV
              FLQNAKTLLKKISEASKAFQMEKIEHGYENMNHFTVNINREKKIIREIDFYREDEDEE
              EBEGGEGKEEEGEVGGEAVEVEVENVQTEFPGEDENPEKASELSQVELQAAPGALP
              VSSPEPPALPPAADAPVTQGEVVPTCSGEQTTESEITPVPAAAETADDLFYSSWYKQOT
              RXATTNPPCTPGSSEGLGQIGPPGSSEDSNVRKAEVAPAAAASERAAVSGKETSAPAATSQ
              ELVICLALLAFILLHYIWSQIQCLIFIMDWI"
ORIGIN
      Query Match     43.7%;  Score 1131.6;  DB 9;  Length 1960;
      Best Local Similarity   84.5%;  Pred No. 1.7e-275;
      Matches 1304;  Conservative    0;  Mismatches 219;  Indels   21;  Gaps   2;
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(Sequence alignment region — Query (Qy) and Database (Db) paired lines)

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Qy     66  GGGACAGCGCAAGGAAATGAGCACTTCTCGAATTACAAGTCTTTCTCCAAGAGCAGCAGA  125
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Db    213  GGGACAGCGAGGAGATGAGCGGCATCTCTGAATTACAAATCTTTTTTCCAAAGAGCAGCAGA  272

Qy    126  CCATGGATAACTTGGAAAAAGCAACTGACTTGTCTCCATCTGCCTACAGAGAGTTCACGAAGC  185
           |||||||||||||||| ||| |||||||||||||||||||||||||||||| |||||||
Db    273  CCATGGATAACTTAGAGAAGCAACTCATCTGTCCCCATCTGCCTTAGAGATGTTCACGAAAC  332

Qy    186  CTGTGGTCAATCTCCCTTGCCAGCACAACCTGTGCAGGAAAAGTGCCAGTGACATCTTCC  245
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Db    333  CTGTGGTGAATCTCCCTTGTCAGCACAACCTGTGTAGGAAAGTGTGCCAGTGAATATTTCC  392

Qy    246  AGGGCCTCTAACCCGTTACCCAGAAGACGCACCACCGTGGCATGCCAGAGAGTTCACGAAGC  305
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Db    393  AGGGCCTCTAACCCGTATTTGCCCACAAAGACGAGGTACCACCATGGCATCAGGGGGCGGAT  452

Qy    306  TCCGGCTGTGCCCTCCTGCAGACATGAGGTGGTGTTGAGACAGAACATGAGGGGTCTATGGGACTGC  365
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Db    453  TCCGGCTGCCCATCCTGTAGACATGGAGTTGGTTTTGGGATAGACATGGGTATATGGGACTTC  512

Qy    366  AGAGGAACCTGCTCGTGGAAAACATTATTGATATATTACAAGCAGCAGAATCCAGCGCCAG  425
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Db    513  AGAGGAACCTGCTGGTGGAAATATCATTGACATCTACAAGCAGAGTCCACCGCCAGGGTT  572

Qy    426  AAAAGAAATTGGACACGACCCCATGTGTGAAGAGCATGAAGAACACGCATCAACATCTATT  485
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Db    573  AAAAGAAAATCCGACCAGCCCATTGTGCAGGAACATGAAGAGGAACGCATCAACATCTACT  632

Qy    486  GTCTGAACTGTGAAGTGCCCACCGTTTCCTTGTGCAAGGTTTTTGGCGCCCATAAGGACT  545
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Db    633  GTCTGAACTGCGAAGTACCCACCGTCTGTGTTCTGCTCAAGGTGTTTGGTGCACACAGAGACT  692

Qy    546  GCCAGGTGGCTCCCCTGACTCATGTGTTCAGAGCGAGAGCTCAGCGTAGTCAGTGGTA  605
           |||||||||||||||||||||||||||| ||||||| |||||||||||||||||||||
Db    693  GCCAGGTGGCTCCCCTGCATTCATGTGTTCCAGAGACAGAGTCTCAGCCTGATGGAGGGCA  752

Qy    606  TTGCTGCTACTTGTGGGGAAGCAACGATAGAGTCCAGGGTGTGATCAGCCTGGAGGACA  665
           |||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    753  TCGCCATCCTCGTGGGCAGCAACGATCGCGAGGTGCAGCAAGTGATCAGCCAGCTGGAAGACA  812

Qy    666  CCTGTAAAACTATTCTGAAGAAGTTGCTGCAGAAAGCAGAAAACAGGACTCTGTGTGAAAATTTG  725
           ||||| |||| |||| |||||||||| |||||||||||||||||||||||||||||||||
Db    813  CCTGCAAAACTATTCGAGGAGAATGTTCGGCAGAAAACAAGAGGACTTTGTTGAGAAGTTTG  872

Qy    726  ATCACCTATACGGCATCCTGGAGGAAAATGACCCAAGCCATCACTCACTCGAA  785
           || |||||| ||| |||| ||||||||||| || |||||||| |||||||||||
Db    873  ATTACCTGTATGGCATTTTGGAGGAGAAAATGAAAAATGAAATGACCCAAGTCATTACCCGGAA  932

Qy    786  CACAGGAGGAGGAAAACTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCACCTGG  845
           ||||||| | |||| ||||||||||||| |||||| ||||||| |||||||||
```

(continued alignment)

```
Qy   1086  CAGGAG------------------------------AAATAGATGAAGAGAGAGAGGAGGAGGATCCAGTAGAAG  1130
           ||||||                              |||| |||| |||| |||||||||||||||||||||
Db   1233  AAGAGAGGGCGGAGAAGAAGATGGTCGGAAGAAAGAAGAGAAAGGAAGAAGAGTGGGACAGTAGAAG  1292

Qy   1131  TAGACAGAGGCAGAAAATGTTCAAATAGCATCTTCAGGGAGGAGAAGTCTGGGACAG  1190
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Db   1293  TGGAGAGAGTTGAGAAAATGTTCAAAACAGAGTTCCCAGGAGAGAGATGAAAAACCCAGAAAAAG  1352

Qy   1191  CTGCAGAGGCCCTCTCCAGCTTCCCGCAGCTTCACGTCGCCCAGAGAGAAGATGAAAACTCGCTT  1250
           ||||| |||||| ||||||| |||||||||||||| | |||| ||||| ||||||| ||||||
Db   1353  CTTCAGAGCTCTTCCAGGTG------------GAGCTGCAGGCTGCCCCTGCACTTCCAGTTT  1406

Qy   1251  CCTCTCCAGGACCGTTTTTGTCATCCATGCCACCACCGTGCTGCAGTGTTTGGTCTTGGGTGTACACCA  1310
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Db   1407  CAGAAACTGCGGATCCCTGTTTTTACCCAGTTGGTTATAAAGGCCAAAACCGGAAAGCCA  1466

Qy   1311  AGGTGGTGCCCCATTGGCTCTCAGACATGGGAGTGGAAAGTGAAAGGCCTCAGCAG  1370
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Db   1467  AGGTTGTACCCACCGGCTCTGAGCGAGGACAGCAGTGTCGAAGAACTCCAGTGTCTGAACTGCGAG  1526

Qy   1371  CGGGAAACTGCGGGGATCCCTGTTTTTTATCCCCTAGTTGGTTGTTGTATATAAAAGGCCAAAACCA  1430
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Db   1527  CAGAAACTGCGATCCCTGTTTTTTACCCAGTTGGTTATAAAGGCCAAAACCCGGAAAGCAG  1586

Qy   1431  GCTCCAAACCCACCTTGCACTCCATGGGAGGTGAAAGTGTCGAAGAGGGCCTCAGCCAG  1490
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Db   1587  CCACCCAACCCACCCTTGCACTCCCCAGGAGCGCGAAAGTGTCGGGGGCCTTCCAGGTT  1646

Qy   1491  TTGAGGATTTCCAGTGGTGCAGTCCCGACGAAGTGGCAGAAGCGCCACCAATGAGCAGGCAG  1550
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Db   1647  CTGAGGATTCGCAAATGTACGGAAAGGCAGAAGTGGCAGCAGCCGAGTGAAGAGAGGCAG  1706

Qy   1551  CAGTGAGTGGTGTAAGGAGTGTTAGTTCAAACTGCAGAGCTACCCTCTCAG  1594
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(right-hand side continued alignment block)

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Qy    906  TATTTCTGCGAATGCCAAGACCCGTGTTGCAAAAAGATCGTTGGAAGGCATCAAAGGGCGTTTC  965
Db   1053  TGTTTCTGCAGAATGCCAAAACCCTGCTAAAAAAAATCTCGGAAGACCATTTC  1112
Qy    966  AGATGCGAGAAACTAGAACAAGAGGTTATGAGATCATGAGCAACTTCACTGTCATCATCAGAATTCCAATA  1025
Db   1113  AGATGGGAGAAATAGGAACATGAGGCTATGAGAACAATGGGAACACAACCACTTCACAGTCAATA  1172
Qy   1026  GAGAAGAAAAAATATTCCGTGAAAATTGACTTTTTCTCAGAGAGAAGAGAGAGAAGAGAGAAGAGGAAGAAGATG  1085
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```
AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
          Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
          Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
          Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
          Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
          Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
          Graham,J., Grand-Pierre,N., Hafez,N.,
          Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
          Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
          Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
          Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
          Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
          Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
          O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
          Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
          Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
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          Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
          Vassiliev,H., Venkataraman,V.S., Viel,I., Vo,A., Wilson,B., Wu,X.,
          Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE     Direct Submission
JOURNAL   Submitted (10-MAR-2003) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3  (bases 1 to 227536)
AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
          Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
          Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
          Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
          DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
          Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
          Galagan,J., Gardyna,S., Graham,J., Grand-Pierre,N., Hafez,N.,
          Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
          Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
          Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Lui,A., Mabbitt,R.,
          MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
          McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
          Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
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          Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
          Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
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          Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,I.,
          Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
          Zimmer,A. and Zody,M.
TITLE     Direct Submission
JOURNAL   Submitted (01-OCT-2004) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT   On Sep 27, 2004 this sequence version replaced gi:52694042.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html
          ------------------------ Genome Center
          Center: Whitehead Institute/MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence_submissions@broad.mit.edu
          ------------------------ Project Information
          Center project name: L19666
          Center clone name: 199_M_5
          ------------------------
        * NOTE: This is a 'working draft' sequence. It currently
        * consists of 6 contigs. The true order of the pieces
        * is not known and their order in this sequence record is
        * arbitrary. Gaps between the contigs are represented as
        * runs of N, but the exact sizes of the gaps are unknown.
        * This record will be updated with the finished sequence
        * as soon as it is available and the accession number will
        * be preserved.
        *
        *         1       7177: contig of 7177 bp in length
        *      7178       7277: gap of unknown length
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     *         92479      92578: gap of unknown length
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     *        187578     187677: gap of unknown length
     *        187678     227536: contig of 39859 bp in length.

ORIGIN
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        Matches 1006; Conservative   0; Mismatches  16;  Indels   2;  Gaps   2;
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Qy    1568 TCTTAGTTCAACTGCAGCTACCTTCTCAGATTGGATTTGAGGCCCTTCTCCCCAGGGACAG 1627
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Db  132389 TCTTCATCCACACATTTCTTCTTTTTGCAGATTGGATTTGAGGCCCCTTCTCCCCAGGCAG 132448

Qy    1628 TCTGCAGCCTTGGGGAGTGGGGGGTGGGGG-TGATCCTGAGCGCAGCTCGCGCCACGTGTA 1686
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Qy    1687 TTCTCCTGGTTTGAATTCCCTAAAATGAAATAATATATTTATTCTCGTTGCTGTGCTCTG 1746
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Qy    1807 AGGGGACCTTCTGGACAGGATTTCTGAAAGCAAAACAAATACAACACCACCACCCTT 1866
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Qy    1867 TAAATTCCAGATGACTTATCTCACTCATTGAGAAAAATGAGATTATGCTCAGAACAAAATTACA 1926
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Qy    2047 CAAAGTGGCAGAACACTCTCCCCAGCCGCCTCCCAGGGTTTCTGGTTATTTAGGACGCTTGT 2106
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Qy    2107 GCCTTTTTTGCTTTTTCTCCTTAGCATTGCAGGTGGTAGGTGAGTTCAGTGTTCCAAA 2166
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Db  132928 GCCTTTTTTGCTTTTTCTCCTTAGCATTGCAGGTGGTAGGTGAGTTCAGTGTTCCAAA 132987

Qy    2167 CTGACCGATTTATCAAAAATATGGAGATTGGTCACTGCAGCAAAAGCTATGTAGTGTCACTGTGTA 2226
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Qy    2287 CACACGTCCATAGTCCAGAAGGCCAAAAAATCTTAGGGGACACATTTTTCTTTAAC 2346
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Qy      2467 CTGCATGGATTTAAGTATACACACAACAATTCTCCCCTCTCTCTCTCTCTCTCTCTCTCTC 2526
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Qy      2527 TCCCCCTCTCCCTCGTGTTCTTTCTCTTCTTC 2586
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Qy      2587 CTCC 2590
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RESULT 8

BC007750

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LOCUS       BC007750                1741 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens ring finger protein 29, transcript variant 3, mRNA
            (cDNA clone MGC:12836 IMAGE:4110783), complete cds.
ACCESSION   BC007750
VERSION     BC007750.2  GI:33871581
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1741)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1741)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT   On Aug 19, 2003 this sequence version replaced gi:14043531.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
```

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,A., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,E.D.

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                     NE"
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This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 14916468.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAL Plate: 17 Row: d Column: 4

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        Best Local Similarity      84.2%;    Pred. No. 1.6e-219;
        Matches 1058; Conservative 0; Mismatches 177; Indels 21; Gaps 2;

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RESULT 9
LOCUS       AX746908               2634 bp    mRNA    linear   PAT 20-JUN-2003
DEFINITION  Sequence 433 from Patent EP1308459.
ACCESSION   AX746908
VERSION     AX746908.1  GI:32131296
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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tanechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1308459-A 433 07-MAY-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
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Query Match             35.2%;  Score 910.8;  DB 6;  Length 2634;
Best Local Similarity   84.2%;  Pred. No. 1.6e-219;
Matches 1058;  Conservative     0;  Mismatches 177;  Indels  21;  Gaps   2;
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            similar to Mus musculus RING-finger protein MURF mRNA.
ACCESSION   AK091310
VERSION     AK091310.1  GI:21749650
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2634)
  AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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            Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
            Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
  TITLE     Complete sequencing and characterization of 21,243 full-length
            human cDNAs
  JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
   PUBMED   14702039
REFERENCE   2
  AUTHORS   Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
            Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
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            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2634)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@nri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
     source          1..2634
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DFNES2007332"
                     /cell_type="normal dermal fibroblasts (Neonatal Skin)
                     (NHDF2564)"
                     /clone_lib="DFNES2"
                     /note="cloning vector: pME18SFL3-primary culture, normal
                     dermal fibroblasts"
ORIGIN

Query Match             35.2%;  Score 910.8;  DB 9;  Length 2634;
Best Local Similarity   84.2%;
Matches 1058; Conservative   0; Mismatches 177; Indels  21; Gaps   2;
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Qy         66 GGGACGGCAAGGAAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGAGCAGA 125
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Db        363 GGGACCAGCGAGGAGATGAGCGCATCCTGAATTACAAAATCTTTTTCCAAAAGAGCAGCAGAGA 422

Qy        126 CCATGGATAACTTGGAAAAACCAACTGATCTGTCCCATCTCTGCCTAGAGATGTTCACCGAAGC 185
              ||||||||||||| |||||||||||||||| || |||||||| |||||||||||||||||||||
Db        423 CCATGGATAACTTAGAGAAGCAAACTCATCTGTCCCATCTCGCTTAGAGATGTTCACGGAAAC 482

Qy        186 CTGTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAAATGTGCCACAGTCTTCC 245
              ||||| ||  ||||||||||||||||||| |||||||| || |||| ||||||||| | | |
Db        483 CTGTGGTGATTCTCCCTTGTCAGCACAACCTGTGTAGGAAAATGTGCCAGTGATATTTTCC 542

Qy        246 AGGGCCTCTAACCCGTACTTACCCACAAGAGGAGCCACACCGTGGCCATCAGGGGGCCGCGCT 305
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Db        543 AGGCCTCTAACCCGTATTTGCCCACAAGAGAGGAGTACCACCATCAGGGGGCCATCAGGGGGGAT 602

Qy        306 TCCGCGTCGCCCATCCTCGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTC 365
              |||||| |||||||||||||||||| |||| || ||||||| || ||| ||| ||||| |||
Db        603 TCCGCTGCCCATCCTCGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTC 662

Qy        366 AGAGGAACCTGTCTGTGGAAAACATTATTGATATCTACAAGCAGCAGAATCACCAGGCCAG 425
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Qy    663 AGAGGAACCTGCTGGTGGAAAAATATCATTGACATCTACAAGCAGGAGTCCACCAGGCCAG
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Db    426 AAAAAAAAATTGGACCAGCCCATGTGTGGAAGAAGCATGAAGAGGAACCATCAACATCTATT 485

Qy    723 AAAAGAAAATCCGACACAGCCCATGTGTGGGAGGAAGAACCATCAACATCTACT 782
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Qy    486 GTCTGAACTCGAAGTGCCCAGCCCACCTGTTCCTTGTGCGGCGCCCCATAAGGACT 545
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Db    783 GTCTGAACTCGAAGTGCCCAGCCCACCTGTTCCTTGTGCAGGTGTTGGTCACAGAAGACT 842

Qy    846 AGAACGTATCCAAGTTGGGTGGTGGAGTCAGTTCATTGAGATCATTGAGACCCGAAATGCAG 905
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Qy   1251 CCTCTCCAGAACCGGTTTTCATCCATGCCACCTGGCTCGCAGAGTTCCTTGGTGACACAG 1306
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Db   1503 CTTCAGAGCTCTCTCAG------GTGGGAGCTGCAGCCGTGCCCCTGGGCCACTTCCAGTTT 1556
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ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Iakovenko,A. and Gautel,M.
  TITLE     Titin-associated zinc-finger proteins link titin kinase to
            transcriptional control
  JOURNAL   J. Muscle Res. Cell Motil. 21, 833-833 (2000)
REFERENCE   2
  AUTHORS   Pizon,V., Iakovenko,A., Van Der Ven,P.F., Kelly,R., Fatu,C.,
            Furst,D.O., Karsenti,E. and Gautel,M.
  TITLE     Transient association of titin and myosin with microtubules in
            nascent myofibrils directed by the MURF2 RING-finger protein
  JOURNAL   J. Cell. Sci. 115 (Pt 23), 4469-4482 (2002)
  MEDLINE   22302063
   PUBMED   12414993
REFERENCE   3  (bases 1 to 1810)
  AUTHORS   Gautel,M.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-1999) Gautel M.S., Physikalische Biochemie,
            Max-Planck-Institut fuer molekulare Physiologie, Otto-Hahn-Strasse
            11, Dortmund, 44227, GERMANY
FEATURES             Location/Qualifiers
     source          1..1810
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="cardiomyocyte"
                     /tissue_type="cardiac muscle"
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                     /gene="RNF29"
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                     muscle growth-related signal transduction"
                     /note="50kDa isoform
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                     /product formerly name titin zinc-finger anchoring protein"
                     /codon_start=1
                     /evidence=experimental
                     /product="RING finger protein 29"
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                     NE"
ORIGIN
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RESULT 11
HSA243488
LOCUS       HSA243488               1810 bp    mRNA    linear   PRI 08-NOV-2002
DEFINITION  Homo sapiens RNF29 gene for RING finger protein 29, 50kDa isoform.
ACCESSION   AJ243488
VERSION     AJ243488.1  GI:14588845
KEYWORDS    alternative splicing; MURF2; RING finger protein 29; RNF29 gene;
            signal transduction; titin zinc-finger anchoring protein; tizian.
SOURCE      Homo sapiens (human)
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Query Match     35.1%;  Score 909.2;  DB 9;  Length 1810;
Best Local Similarity   84.2%;
Matches 1057;  Conservative   0;  Mismatches 178;  Indels 21;  Gaps  2;

Qy     66 GGGACCGCAACGGAAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGCAGCAGA 125
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Db    213 GGGACAGCGGAGGAGAATGAGCCCATCTCTGAATTACAAAATCTTTTTTCCAAAGACAGCAGA 272

Qy    126 CCATGGATAACTTGGAAAAGCAAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGC 185
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Db    273 CCATGGATAACTTAGAGAAGGCAAACTCATCTGTCCCATCTGCTTAGAGATGTTCACGAAAC 332

Qy    186 CTGTGTGATCATTCTCCCTTGTCCAGCCACAACCTGTCGCAAGGAATGGTGCCAGTGACACTCTCC 245
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Db    333 CTGTGTGGTTGATTCTCCCTTGTCCAGCACAACCTGTGTAGGGAAAATGTGCCAGTGATATTTCC 392

Qy    246 AGGCCTCTAACCGTACTTACCCACAAGAGGAGGAGGACCACCGTGGGATCAGGGGGGCGGCT 305
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RESULT 12

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Db    393  AGGGCCTCTRAACCCGTATTTGCTCAACAAGAGGAGGTRACCACCATGGCATCAGGGGGCGGAT
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Qy    306  TCCCGCTGCCCTCCTTCCTGCAGATCAGAGGGGTCTTATGGACTGC 365

Db    453  TCCCGCTGCCCATCCCTGTAGACATGAAGTGGTTTGGATAGACATGGGACTTC 512
Qy    366  AGAGGAAACCTGCTCGTTGGAAAAACATTATTGATATATCTACACAAGCACGGAATCCACCAGGCCAG 425

Db    513  AGAGGAAACCTGCTGGTGGGGAAAATATCATTGACACTACACAAGCACGAGAGTGTTCCACCAGGCCAG 572
Qy    426  AAAAAAAATTGGACACGACCCCAGTGTGTGAGAGATGAAGAGGAAGGCCATCAACATCTATT 485

Db    573  AAAAAGAAAATCCGACACCAGCCCATGTGCGAGGAACATGAAGGACGCGATTCTACT 632
Qy    486  GTCTGAACTGTGAAGTGAACGTGCCCACCTGTTCCTTGTTGTGGCGCCCATAAGGACT 545

Db    633  GTCTGAACTGCGAGTACCCCACCTGCTCTCTGTGTGGTCGCACACAGAGACT 692
Qy    546  GCCAGGTGGCCTGCCCCCTGACTCAGTGTTGCGAGGACAGAGCTTCAGTGATGGTA 605

Db    693  GCCAGGTGGCCTGCCCCTCACTCATGTGTTCCAGGACACAGAAGTCTGAGCTGATGGCA 752
Qy    606  TTGCTGTACTTGTGTGGGAAGCAGACGATTAGAGTGCAGCTGCAGGGTGTTGATCAGGTGAGGGACA 665

Db    753  TCGGCCATCCTTCGGTGCCCAGGCAGGACAAACGATCAGAGCTGGAGTGCATCAGGCCAACGATGAAGACA 812
Qy    666  CCTGTAAAACTATTGAGGAGTTCGCTGCAGAAAGCAGGACAACGTGTGTGAGAGAAAATTTG 725

Db    813  CCTCCAAAAACTATCCAGGAATGTTCCAGAAAACAAGAGCTTTGTTGGAAGTTTG 872
Qy    726  ATCACCTATACGGCATCCTGGAGGAGGAGAGAGGACTGAAAAATGACCCAAGCCATCACTCACTCGAA 785

Db    873  ATTACCTGTRATGGCATTTTGGAGGAGGAAGGAATGAAATGAGACCCAAGTCATTACCCGAA 932
Qy    786  CACAGGAGGAGGAGAGAACTGGGACATGTCCGAACTCTTATCAGGATRATTCCGATCACCTGG 845

Db    933  CCCAAGAGGAGGAGAAACTGGAACAGTGTCCGGTGCCTCTGATCAAAAAGTATTCTGATCATTTGG 992
Qy    846  AGAACGTATCCAAGTTGGGGTGGGAGTGCAGGAGTCCAGTTGTTCATTGGATGAGCTGCAGGAAATTG 905

Db    993  AGAACGTCTCAAAGTTGGTTGAGTCAGGAGTTCAGTTTAATGGATGAGCCAGAATGGCAG 1052
Qy    906  TATTTCTGCAGAATGCCAAGACCCTGTTTGCAAAGATGTCTGGAAGCATCAAAAGGCGTTTC 965

Db    1053 TGTTTCTGCAGAATGCCAAAACCCTGCTAAAAAAATCTCGGAAGCATCAAAAGGCATTTC 1112
Qy    966  AGATGGAGAAACTAGAACAAGGTTATGAGAGTCATGAGAAAG 1025

Db    1113 AGATGGAGAAAATAGAACATGGCTATGAAGCATGAACAGAAACCACTTCACAGTCAACCTCAATA 1172
Qy    1026 GAGGAGAAAAAAAATTATCCCGTGAAATTGACACTTCTCTAGAGGAGAGGAGGAAGAGATG 1085

Db    1173 GAGAGAGAAAAAGATAATAACGTGAAAATTGACAGTTTACAGAGGAAGATGAAGAAGAAGAG 1232
Qy    1086 CAGGAG------------AAATAGATGAAGAAGGAGGAAGGAGAAGAGGCAGTAGAAG 1130

Db    1233 AAGGAAGGGCGGGAGGAGGAAGAGTGGGAGGAGGAAGCAGTAGAAG 1292
Qy    1131 TAGAAGAGAGGCCAGAAAATGTTCAAATAGCATCTTCAGGGAGGGAAGAGTCTGGAGAAG 1190

Db    1293 TGGAAGAGGAGGTTAGAAAATGTTCAAACAGAGTTTCAGCGGAGAAGATGAAAAACCAGAGAAAG 1352
Qy    1191 CTGCAGAGAGCCCCTCCACAGCTTCCCCGAGAGCTTCAGGTCGCCCCCCCAGAGCGACTTCACTTGCTT 1250

Db    1353 CTTCAGAGAGCTCTCTCAG------GTGGAGCTGCAGGCTGCCCTGCCCCAGAGCCACTTCCAGTTT 1406
Qy    1251 CCTCTCCCAGAACCGTTTTCATCCAATGCCACACTGCTGCAGATGCGTCGCCAGTCGTTGACACAG 1306

Db    1407 CCTCTCCCAGAGCCCCAGCGCCACCTGCTGCCACCTGCTGCGCAGAATGCCCCTGTGCACACAG 1462
Qy    1407 ... 
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RESULT 13
BT008253

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Db  121  GCCTCTAACCCGTATTGCCCACAAGAGGAGGTACCACCATGGCATCAGGGGGGCCGATTC 180
Qy  308  CGCTCGTCTCCTTCCTTGCCTTGCTGCGACACAGAGGTGGTGGTTAGCAGACATGGGGTCTCATGGACTGCAG 367
Db  181  CGCTCGCCCATCCTGTAGACATTGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTCAG 240
Qy  368  AGGGAACCTTGCTTCGGTCTGGGAAAAACATTATTGATATCTACAAGCAGCAGGAGGCCAGAA 427
Db  241  AGGAACCTGCTGTTGGTGAAAATATCATTGACATTCAAAGCAGCAGGAGGCCACCAGGGCCAGAA 300
Qy  428  AAAAAATTGGACCAGCCATGTGTGAAGAGCAGCATGAAGAGCAACATCTATTGT 487
Db  301  AAGAAATCCGACCAGCCAGCCCCATGTGCGAGAGAACATGAAGAGCCGCATCAACATCTACTGT 360
Qy  488  CTGAACTGTGAAGTGCCCACCTGTTCCTTGTCGCAAGGTTTTGTGGGGCCCATAAGGACTGC 547
Db  361  CTGAACTGCGAAGTACCCACCTGCTCTCTGTCGCAAGGTCGTTTGTGGTCACACAAAGACTGC 420
Qy  548  CAGGGTGGCTCCCCTGACTACCATGTGTTCCAGGGTCAGAAGTCAGAGTCTCAGTCGTATT 607
Db  421  CAGGGTGGCTCCCCTCACTCAGTGTTCCAGGAGCACAGAAGTCTGAGCTCAGTGATGGCATC 480
Qy  608  GCTGTACTTGTGGGGAGCAAACDATAGAGTCCAGGGTGTGATCACGCTGGACGACC 667
Db  481  GCCAATCCTCGTGGGCCAGCAAGATCAGTCCAGGGAGTGATCAGCTGGAAGACACC 540
Qy  668  TGTAAAAACTATTGAGAGTGCTGCAGAAAAGCAGAAACAGCCTGTGTGAGAAAATTGAT 727
Db  541  TGCAAAAACTATCGAGAGTTGGTTGCAGGAAAACAGAAACAGCCTTTGTGAGGAGTTTGAT 600
Qy  728  CACCTTATACCGGCATCCTCTGGAGGAGAGAGGAGAAGAGCTGAAATGACCCCATCCGAACA 787
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Qy  788  CAGGAGGAGAAACTGGAACATGTCCGAACCTCTTATCAGGAGTATTCCGATCACCTGGAG 847
Db  661  CAAGAGGAGAAACTGGAACATGTCCGTCCGCTCTGATCAAAAGTAATTCTCAATTGGAG 720
Qy  848  AACGTATCCAAGTTGGTTCAGAGTGTCAGGAATCCAGTTCATGTGATGAGCCGAAATGGCAGTA 907
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Qy  908  TTTCTGCAGAATGCCAAGACACCTGTTGCAGAAAAGATCGTGAGAGCATCAAAAGGCGTTTCAG 967
Db  781  TTTCTGCGAAATGCCAAAAACCCTGCTAAAAAAATCTCGGAGGCATCAAAAGGCATTTCAG 840
Qy  968  ATGGAGAAACTAGAACAGAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCAATAGA 1027
Db  841  ATGGAGAAATAGAACATGGCTATGAGAACCACTTCACAGTCAACCTCAACCTAATAGA 900
Qy  1028 GAAGAAAAAITATCCGTGAAATTGACTTTTCTAGAGAAGAGAGAGAGAAGAAGATGCA 1087
Db  901  GAAGAAAAAGATAATACGTGAAAATTGACTTTTACAGAGAAGGATGAAGAAGAAGAA 960
Qy  1088 GGAGAAATAGATGATGAAGGAAGGAAGGAAGAGA 1132
Db  961  GAAGGCGGAGAAGGAGAAGAGAGAGGGGAGGAGAAGAGGAAGAGTG GGATGCAGTAGAAGTA 1020
Qy  1133 GAAGAGGCAGAAAATGTTCAAATAGCATCTTCAGGGGGAAGAGAGTCTGGAGAAAGCT 1192
Db  1021 GAAGAGGTAGAAAGTTCAAACATGGCTATTTCCAGAGAAGAGAAAAACCAGAAAAAGCT 1080
Qy  1193 GCAGAGGCCCCTCAGCTTCCCGGCAGCTTCAGGTGGCGCCCAGAGCGCCACTACCTCGTCC 1252
Db  1081 TCAGAGCTGTCTCTCAG-----GTGGGGACCTGCAGGAGTGTCCCCCTTGCGGGGGCACTTCCAGTTTCC 1134
Qy  1253 TCTTCCAGAGAACCGTTTTCATCCATGCCACCTGTGCAGATGGTTCCTGGTGACACAG 1306
Db  1135 TCTCCAGAGCACCTCCAGCCCTGCGCATGCCAGCCCTGTCCGGATGGTGACACAG 1188
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Qy  1  ATGGATAAACTTGGAAAAAGCAACTGATCGATCTGTCCATCTGCCTGAGAGAGTTCACGAAGCCT 60
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Qy  61 GTGGTGATTCTCCCTTGTCAGCACAACCCTGTGTAGGAAAATGTGCCAGTGATATTTTCAG 120
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RESULT 14

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Qy    121 GCCTCTAACCCGTATTCGCCACAAGAGGAGGTACCACCATGGCATCAGGGGGCCGATTC 180
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Db    121 GCCTCTAACCCGTATTCGCCACAAGAGGAGGTACCACCATGGCATCAGGGGGCCGATTC 180

Qy    181 CGCTGCCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTCAG 240
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Db    181 CGCTGCCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGACTTCAG 240

Qy    241 AGGAACCTGCTTGGTGGGAAAAATATCATTGACATCTACAAGGACGAGTTCAACCTGGAA 300
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Qy    301 CTGAACTGGTGGAAGTACCCACCTCACCTGCTCTCTGTGCAAGGGTTTTGGCGCCCATCA 360
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Db    301 CTGAACTGGTGGAAGTACCCACCTCACCTGCTCTCTGTGCAAGGGTTTTGGCGCCCATCA 360

Qy    361 CTGAACTGGCGGAAGTACCCACCTCGTCAAGGGTGTTTGGTGCACAGAAGACTGC 420
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Db    361 CTGAACTGGCGGAAGTACCCACCTCGTCAAGGGTGTTTGGTGCACAGAAGACTGC 420
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Best Local Similarity   75.8%;  Pred. No. 3e-167;
Matches  872;  Conservative   0;  Mismatches  279;  Indels    0;  Gaps    0;
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Qy    140 GAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAGAGCCTGTGGTGCATTCTC 199
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Qy    320 TGCAGGACATGAGGTGGTGGTTAGACAGACATGGGGTCTATGGACTTCAGGGAGAACTGCTC 379
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Db    363 TGCAGGCATGAAGTGGTGTCCTCGACACCGGCACGGGGCTCCAGACACCGAGTTACGGCTCC 422

Qy    380 GTGGAAAACATTATTGATATATCTACAAGCAGAATCCACAGGCCAGGAAAAATTGGAC 439
          ||||| |||||||| ||||| | ||||| ||||||||||| ||||| ||||| |||
Db    423 GTGGAGAACATCATTGATTATATATACAAGGCCATCAACAACATCTATTTGTTCGAACTGTGAACTGGGAC 482

Qy    440 CAGCCCATGTGTGAAGAGCATGAAGAACGAAGGCCATCAACACTTATTTGTTCTGAAACTGGAA 499
          |||||||||||||| ||| ||||| |||||||||||||||||||||||| |||||||||||||
Db    483 CTGCCAAATGTGCGAAGAGCATGAAGAAGATGAGAAGATCAATATCTATTTGTTTGAACTGTGAA 542
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Qy    428 AAAAAATTGGACAGCCCATCAGTGTGAAGAGCGATGAGGCCATCAACACATCTATTGT 487
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAGGTGGCTTCCCCTGACTCATGTCTTCCAGAGGGTCAGACTCAGTCAGTGATGGTATT 480

Qy    488 CTGAAACTGTGAAGTGCCCACCACCTGTTCCTTGTGCAAGGGTTTTTGGCGCCCATCA 547
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCATCTCGTGGGCAGCAACGATCGAGTCAGCAGGAGTGATCAGCCTGGAGAGACACC 540

Qy    548 CAGGTGGCCTTCCCCCTGACTCATGTCTTCCAGAGGGTCAGACTCAGTCAGTGATGGTATT 607
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCAAAACTTATCGAGGAATGTTGCAGAAAACAGAAAGCAAGAGCTTTGTGTGGAAGTTGGAG 600

Qy    608 GCTCTACTTGTGGGAAGCAACGATAGAGTCCAGGGTGTGACTGAGGGGACACC 667
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TACCTGTATGGCATTTGGAGTCGAGCTGAGAATTGAGTCTTTATGGAGCATGTCATTACCCGGAACC 660

Qy    668 TGTAAAACTATTGAGGAGTGCTGCTTGCAGAAAAGCAGAAACAGGACTGTGTGTGAGAAATTTGAT 727
          ||| |||| ||||||| |||||||||||| |||||||||||||||| ||||||||||||||||||
Db    661 CAAGAGGAGGAACTGGAAGTCGGTGCTCTGATCAAAAAAGTATTCCCGATCATTTTGAG 720

Qy    728 CACCTTATACGGGCACTCCTCGGAGGGCACGTGAAAATGACCCAAGTCAAAGGGCAGTG 787
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTCTCAAAAGTTGGTTGAGTCAGGAAATTCAGTTTATGGATGAGGCCAGAAATGGCAGTG 780

Qy    788 CAGGAGGAGGAAACTGGAAACATGTCCGGAACTCTTATCAGGAAGTATTTTCCGATCACCTGGAG 847
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Db    781 TTTCTGCAGAATGCCAAACCCTGCTAAAAAATCTCGGAACCATCAAAAGGCATTTCAG 840

Qy    848 AACGTATCCAAGTTGGTTGGGTCAGTTCATGGTATGGAGAGCCCGAAATGGCAGTA 907
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Db    841 ATGGAGAAAAATAATTATTGACTTTTCTAGAGAACCACTTCACAGTTCAATAGA 900

Qy    908 TTTCTGCAGAATGCCAAGAGCCATCATGGTCAGGAATTCGTGGGAACGCATCAAAAGGCGTTTCAG 967
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Db    901 GAAGGAAAAGATAATACGTGAAATTGACTTTTACAGAGAGAGAGAAGAGAGGAGAA 960

Qy    968 ATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCAATAGA 1027
          ||||||||||| | ||||||||||||||||||||||||| || ||||||||||||||||
Db    961 GAAGGGAGGCGAGAAGAGAAAGTGGGAGGAGAAGTCGGAGGAGAAGTG 1020

Qy   1028 GAAGAAAAATTATCCGTGAAATTTCTAGAGAAGAGAAGAGAAGAGAAGATCA 1087
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Db   1021 GAAGAGGGTAGAAAAATGTTCAAAACAGAGAAAACCCAGAGAAAAAGCT 1080

Qy   1088 GGAGAAATAGATGAAGAAGAAGGAGAAGGAGA------GGATGCAGTAGAAGTA 1132
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Db   1081 TCAGAGCTCTCAG------GTGGAGCTGCAGGCTGCCCCTGGGCACTTCCAGTTTCC 1134

Qy   1133 GAAGAGGCGAGAAGTGCAGAAAATGTTCAAAATGCATCTTCAGGAGTCTGGACAAGAGCT 1192
          |||||||||||||||||| |||| ||||||||||||||| |||||||||||||||||||
Db   1135 TCTCCAGAGGACGCACCTCAGCCCGCCGCACCTGCTGCGGGATGCCCCTGTGACACAG 1188

Qy   1193 GCAGAGACGCCCTCTCCAGCTTCCCGCGAGAGCTTCAGGTGTCGCCCCCAGAGCCACTACCTGCTTCC 1252
          ||||| |||||||||||||||||||||||||||||||| |||||||||| |||||||||
Db   1188 ...

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RESULT 15

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LOCUS       AC133956              171261 bp    DNA     linear   ROD 01-JAN-2004
DEFINITION  Mus musculus BAC clone RP23-347E10 from chromosome 16, complete
            sequence.
ACCESSION   AC133956
VERSION     AC133956.4  GI:38524721
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 171261)
  AUTHORS   Belter,E., Bielicki,L., Elliott,G. and Haakenson,W.
  TITLE     The sequence of Mus musculus BAC clone RP23-347E10
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 171261)
  AUTHORS   Wilson,R.
  TITLE     Sequencing of Mus musculus
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 171261)
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COMMENT     On Nov 26, 2003 this sequence version replaced gi:35070665.
            -------------- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Summary Statistics
            Center project name: M_BA0347E10
            --------------

            NOTICE: This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.
            --------------

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. Wes Warren,
            Department of Genetics, Washington University, St. Louis MO. For
            additional information about the map position of this sequence, see
            http://genome.wustl.edu

            SOURCE INFORMATION:
            The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa
            and Minako Tateno in the laboratory of Pieter de Jong
            (http://www.chori.org) from female C57BL/6J mouse kidney and/or
            brain genomic DNA.  The clone and detailed information can be
            obtained from Research Genetics, Inc. (http://www.resgen.com) or
            Pieter de Jong and coworkers at http://www.chori.org

            NEIGHBORING SEQUENCE INFORMATION:
            This sequence is the entire insert of the clone. This clone is
            overlapped by AC138605 and AC122837.
FEATURES             Location/Qualifiers
     source          1..171261
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="16"
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                     /clone_lib="RPCI-23"
     repeat_region   75..197
                     /rpt_family="ERVK"
     repeat_region   2099..2179
                     /rpt_family="L1"
     repeat_region   5326..5460
                     /rpt_family="L1"
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Db   543 ATACCCACCTCCTTGTGGTGCCACAAAAGACTCTCAGGTTGCTCCT 602
         ||||||||||||||||||||||||||||||||||||||||||||||
Qy   560 CTGACTCATGTGTTCCAGAGGGCAGAAGTCAGAGCTCAGAGGTTGCTGTACTTGTG 619

Db   603 CTCACAAACGTTTACCAGCAGCAGAAGTCCGAGCTGCAGCATCGGCATCCGAGTCCTGGTG 662
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   560 CTGACTCATGTGTTCCAGAGGGCAGAAGTCAGAGCTCAGAGGTTGCTGTACTTGTG 619

Db   663 GGCACGAATGACAGAGTACAACAGGGATAGTCACGCAGGTGGGAGGGACCTGCAAGACAGTT 722
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   620 GGAAGCAACGATGAGACTCCAGGGTGTGATCAGCAGGACACCTGTAAAACTATT 679

Db   723 GAGGAATGCAGCAGACGACAGAGGAGCAGCTGTGTGTGAAAAATTTGATTTATCTCTATTCT 782
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Qy   680 GAGGAGTGCTGCAGAAAGCAGAAAACAGGACCTGTGTGAGAAAATTTGATCACCTATACGGC 739

Db   783 GTACTCGGAGAGAGAGAAAAAATGAGATGACACAAATAATCACTAGGAACCCAAGAGAGAAA 842
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   740 ATCCTTGGAGGAGGAGGAGGAGACTGAAAATGACCCAAGCCATCACTCACTGAACACAGGAGGAGAA 799

Db   843 CTGGAACATGTCCGGCTCCCTGATGAGAGAAGTATAGCGGAGTGCTGTGTCTAAG 902
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   800 CTGGAACATGTCCGGAACTCTTATCAGGAAGTATTCCGATCACCTGAGGAGACGTATCCAAG 859

Db   903 CTGGTAGAGTCAGGAATCCAGTTCATCGGAACATGGGAGGAAT 962
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Qy   860 TTGGTGGGAGTCAGGAATCCAGTTCATTGGGATGGGCCGGAAATGGGCAGTATTTCTGCAGAAT 919

Db   963 GCAAAAAACAATTGCTCCAAAAAATTACTGAAGCATCTCAAAAGGATTTCAGATGGAAAAATTA 1022
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Qy   920 GCCAAGACCCTGTTGCAAAAAGATCGTGTTGGGAAGCCATCAAAGGGTTTCAGAGTGAGAAACTA 979

Db 1023 GAAGACGGGTATGAAAAATATGAAACCAAATTCACAGTGGAAGAACCTAAGAGAAAAAGATA 1082
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Qy   980 GAACAAGGTTATGAGAGTCATGAGCAACTTCACTGTGTCAAATCTCAATAGAGAAGAAAAATT 1039

Db 1083 ATACGGAGAAATTGATTTTGACAGAGGAAGAGGAGGCGAAGAGAAGTATTAGAGAGACAGTA 1142
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Qy 1040 ATCCGTGAAAATGACTTTTCTTAGAGAAAGAGGGGAAGAGCAGAAGAAAGATGAGAAAATAGAT 1099

Db 1143 GAAGGGGAAGGAGATCTCGGATGAAGTTCACACGAGTCATCGGGAGAGGGAAGAGGGAAGGA 1202
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Qy 1100 GAAGAGGAAGGAGGAGGGGGGATGCAGTTAGAGTAGAGAAAGGGCAGAAAAAGTTCAAAAATAGCA 1159

Db 1203 GAGAAGGAGGAGGAGAGCTGAAAGAGGCACACAGCAGGGAGGACCCTGAA 1262
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Db 1263 CAGCAGAAATGC 1273
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Qy 1220 CTTCAGGTCGC 1230

OM nucleic - nucleic search, using sw model

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                         GenCore version 5.1.6
                         Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:          June 14, 2005, 20:19:07 ; Search time 443 Seconds
                                             (without alignments)
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Perfect score:   2590
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Scoring table:   IDENTITY NUC
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Searched:        1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2590	100.0	2590	3	US-09-908-988B-3	Sequence 3, Appli
2	485.6	18.7	1757	4	US-09-484-970B-37	Sequence 37, Appli
3	450.8	17.4	1431	4	US-09-908-988B-1	Sequence 1, Appli
4	432.2	16.7	1597	4	US-09-908-988B-5	Sequence 5, Appli
5	103	4.0	4867	4	US-09-949-016-13746	Sequence 13746, A
6	82	3.2	7218	1	US-08-232-463-14	Sequence 14, Appl
7	73.6	2.8	4843	4	US-09-949-016-15195	Sequence 15195, A
8	71.2	2.7	64309	4	US-09-949-016-14581	Sequence 14581, A
9	69.8	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
10	64.4	2.5	150394	4	US-09-949-016-13042	Sequence 13042, A
11	63.4	2.4	929	4	US-09-671-317-14	Sequence 14, Appl
12	63.4	2.4	1001	4	US-09-671-317-439	Sequence 439, App
13	63.4	2.4	7044	4	US-09-949-016-14113	Sequence 14113, A
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17	61.8	2.4	49931	4	US-09-949-016-13727	Sequence 13727, A
18	61.8	2.4	49931	4	US-09-949-016-13728	Sequence 13728, A
19	61.8	2.4	49931	4	US-09-949-016-13729	Sequence 13729, A
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24	60	2.3	601	4	US-09-949-016-90371	Sequence 90371, A
25	60	2.3	601	4	US-09-949-016-90372	Sequence 90372, A
26	60	2.3	3117	4	US-09-614-221A-275	Sequence 275, App
27	58.8	2.3	18798	4	US-09-949-016-14339	Sequence 14339, A
28	58.4	2.3	43795	3	US-08-742-185-101	Sequence 101, App
29	58.4	2.3	92227	4	US-09-949-016-11929	Sequence 11929, A
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31	57.2	2.2	16442	4	US-08-781-891-208	Sequence 208, App
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33	56.6	2.2	36156	4	US-09-949-016-12128	Sequence 12128, A
34	56.6	2.2	36156	4	US-09-949-016-13261	Sequence 13261, A
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ALIGNMENTS

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RESULT 1
US-09-908-988B-3
; Sequence 3, Application US/09908988B
; Patent No. 6740751
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1714)
US-09-908-988B-3

Query Match             100.0%;  Score 2590;  DB 4;  Length 2590;
Best Local Similarity   100.0%;
Matches 2590; Conservative    0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 CTCGAGATTTACCCTTACAGAAGCTGTTCGGGAGGCACCTTCCCTTGGCGAGCACACTCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCGAGATTTACCCTTACAGAAGCTGTTCGGGAGGCACCTTCCCTTGGCGAGCACACTCAG 60

Qy         61 GGACAGGGACGGCCAAGGAAAATGAGCACTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120
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Qy        181 GAAGCCTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGCCTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACAT 240

Qy        241 CTTCCAGGCCTTCTAACCCGTACTTACCCACCAAAGAGGACCACCCGTGGCATCAGGGGG 300
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Qy    361 ACTGCAGGAGGAACCTGCTCCGTGGGAAAACATTATTGATAATCTACAAGCAGGAATCCACCAG 420
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[DNA sequence alignment continues — Qy/Db sequence pairs with identity bars from position 301 through 2520]

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Qy  2581 TTCTTCCTCC 2590
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RESULT 2
US-09-484-970B-37
Sequence 37, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
SEQ ID NO 37
; LENGTH: 1757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 247384.1CB1
US-09-484-970B-37

Query Match   18.7%; Score 485.6; DB 3; Length 1757;
Best Local Similarity   67.7%; Pred. No. 7.5e-128;
Matches   696; Conservative   0; Mismatches 329; Indels   3; Gaps   1;

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Db   148 CCAGGATGGGAAATCCCATGGAGAACTTGGAGAAGCAGTCGATCTCGGCCCTPATCTGCCTGGA 207

Qy   172 GATGTTCACGAAGCCTGTGGTCATTCTCCTTGCACGCACCAACCTGTTGCAGGAAATGTGC 231
         |||||| || |||||  ||| |||| | || || | |||||||| ||||| |||| ||||
Db   208 GATGTTTACCAAGCCAGTGTGTCATCTTGCGTGCCAGCACCAACTTGTTGCGGAAGTGTGC 267

Qy   232 CAGTGACATCTTCCAGGCCTTCTAACCTGTACTTACCCACAAGAGGAGGCACCACCCTGGC 291
         ||  ||||| |||||||||||||||||||| || |||||||||||||||| |||||| |||
Db   268 CAATGATATTTTTCCAGGCCTTCTAACCTGTATTTGCCCACAAGAGGAGGTACCACCATGGC 327

Qy   292 ATCAGGGGGCGCCGCTTCCGTCTCCCTCCTCAGACATGAGGTGGTGTTGACACGACACATGG 351
         |||||||||||  || ||||| | || ||| |||||||| ||||| || | || ||||||||
Db   328 ATCAGGGGGCGGCCGATTCCGCTGCCCATCCTGTAGACATGAAGTGGTTTGGATAGACATGG 387

Qy   352 GGTCTATGGACTGCAGAGGAACCTGCTCGTGTGGAAAACATTATTGATATCTACACAGCAGGA 411
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Qy   412 ATCCACCA---GGCCAGAAAAAAATTGGACCAGCGCCCATGTGTGGAAGAGCAATGAAGAGGA 468
         ||||| ||    |||| ||||||  |||  |||||| ||   ||||||||||| | ||||||
Db   448 GTCTCCAGTCCGGCCGATGCCCATCCTGGAGAACATCTACAAACAGCAGGAGGTACCACAGA 507

Qy   469 ACGCATCAACAATCTATTGTGTGAACTGTGAAGTGCCCACCTTGTTCCTTGTGCAAGGTTTT 528
         |||| || || ||| |||||||||| |||| ||||| |||||||||||| ||||||||||||
Db   508 GAAAATCAACAATCTACTGTGTCTCACGTGTGCCCACCTTGGTGGTGTCCCATGTGCAAGTGTT 567

Qy   529 TGGCGCCCATAAGGACTGCAGGTGGCCGACTCATGTGTTCCAGAGCGCAGAAGTC 588
         ||| |||||| |||| || |||||||| |||| || ||||| || ||||||| ||
Db   568 TGGGATCCACAAAGGCCTGCGAGGTGGTCTTGCAGAGTTTCAAGGAGGACAAAAGAC 627

Qy   589 AGAGCTCAGTGATTGGTATTGCTGCTTGTTGGGGAAGCAACGGATAGAGAGTCCAGGGTTGTGAT 648
         | || ||||| | |  ||| | |||  ||||||||||| || |||| |||| ||||| ||||||
Db   628 TGAACTGAATAACTGTATCTCCATGCTGTGGTGCGGGGGAATCACCGTGTGCAGGACCATCAT 687

Qy   628 TGAACTGAATAACTGTATCTCCATGCTGTGGTGCGGGGGAATCACCGTGTGCAGGACCATCAT 687
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Qy   769 CCAAGCCATCACTCGAACACAGGAGGAGGAGAAAACTGAAACATGTCCGAACTCTTATCAGGAA 828
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Db   808 GCAGCGGATCACGCACGAGGAGGAGGAGAAAAAGCTTAGCTTCATCGAGGCCCTGAATTCATCCAGCA 867

Qy   829 GTATTCCGATCACCTTGGGAGAACGTATCCAAGTTGGTCAGGAAATCCAGTTCATGGA 888
         ||| ||||||||||   ||||||| || ||||| |||| ||||||||||||| |||||
Db   868 GTACCAGGAGCAGCTGGACAAGTCCACAAAGCTGTGGAAAACTGCCAGTCCCTGGA 927

Qy   889 TGAGCCGGAAATGGGAGTATTTCTGCAGAATGCCAAGACCCCTGTTGCAAAGATCGTGGA 948
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Qy   949 AGCATCAAAGCGTTTCAGATGGACGAAAACTAGAACAAAGGTTATGAGATCATGAGCAACTT 1008
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Db   988 AGCTTCCAAGGCTGCCAGTGGGGAAGACAGAGCAGGGCGTTTGAGAACATTGACACTTCTT 1047

Qy  1009 CACTGTCAATCTCAATAGAGGAAGAAAAAATTATCCGTGAAAATTGACATTTTCTAGAGAGA 1068
         |||| || || |||| ||| ||||||| |   |||||||||| ||||| |  ||| ||||||
Db  1048 TACTTTGGATTTAGAGCACATAGCAGCGCCCTGAGCCCATTGACTTTGGGACAGATGA 1107

Qy  1069 GGAAGAGGAAGAAGATGCAGGAGAAGTCAGGAAATGAGAAGGAGAAAGGAGGAGGAGGATCGCAGAGAGTAGA 1128
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Db  1108 GGAAGAGGAAGAATTCATTGAAGGAAGAAGAAGAGCAGGAGAGGAAGAGGAAGAGTCCACAGAGGGAA 1167

Qy  1129 AGTAGAAG 1136
         || |||||
Db  1168 GGAAGAAG 1175
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RESULT 3
US-09-908-988B-1
Sequence 1, Application US/09908988B
; Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-09-908-988B-1

Query Match   17.4%; Score 450.8; DB 4; Length 1431;
Best Local Similarity   63.8%; Pred. No. 5.8e-118;
Matches   702; Conservative   0; Mismatches 392; Indels   6; Gaps   1;

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Qy    68 GACGGCGAAGGAAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGAGACC 127
         |||| ||   ||||| || || || || | || |||||| |  | ||||||||||||| ||
Db   187 GAGCGCGCGCGGGATGAACTTCACGTGGGGTTTCAAGGCGTCTAGGGGATGCGACAGAC 246

Qy   128 ATGGATAACTTGGAAAAAGCAACTGATCTGTCCATCTGCCTAGAGAGGTAGAGTTCACGGAAGCCT 187
         |||||| ||| |||| ||||| | ||| ||| ||| | ||| || | ||| |||| || |||||
Db   247 ATGGCAACTTGGAGAAGAGCAGCTCATTTGCCCCATCTGCCTCGGAGATGTTCACGAAGCCC 306
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RESULT 4
US-09-908-988B-5
; Sequence 5, Application US/09908988B

Patent No. 6740751
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION:
; FILE REFERENCE: MYOG:028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 5
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (299)..(1327)
US-09-908-988B-5

Query Match   16.7%; Score 432.2; DB 4; Length 1597;
Best Local Similarity   66.5%; Pred. No. 1.3e-112;
Matches   636; Conservative   0; Mismatches 318; Indels   3; Gaps   1;

[Sequence alignment data — Qy (Query) aligned against Db (Database) sequences with position numbers, spanning positions from ~126 to ~1286]

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Qy   843  TGGAGAACGTATCCAAGTTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAATGG   902
          |||||  |||||         ||||||      |||||     ||||||||||||  ||
Db  1056  TGGAAAGTCCACCAAGCTTGTGGAGACCGCCATCCAGTCCCTCGGATGAGCCCGAGGGG   1115

Qy   903  CAGTATTTCTGCAGRATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGCGT   962
          ||| |  ||||| ||                                       |||
Db  1116  CTACCTTCCTTCTCAAGTGCCCAAGCAGCTCATCAAGCACATTGTAGAAGCCTCCAAGGGCT  1175

Qy   963  TTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCTCA  1022
          |||||                            ||||||||        ||||
Db  1176  GCCAGCTGGGGAAGACAGAGGCAAGGCTTTGAGACATGGACTACTTTACTCTCGACTTAG   1235

Qy  1023  ATAGAGAAGAGAAAAATATCCGTGAAATTGACTTTTCTAGAGAGAGGAGGAGGAGGAG   1079
          |                    |||||||||||||  |||
Db  1236  AACACATAGCAGAGGCCTTGAGGGCCATTGACTTGGGACAGGTGAAAGGATGTGATG   1292
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RESULT 5
US-09-949-016-13746/c
; Sequence 13746, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13746
;   LENGTH: 4867
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13746

Query Match 64.4%; Score 103; DB 4; Length 4867;
Best Local Similarity 64.4%;
Matches 154; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Qy   678  TTGAGGAGTGCTGCAGAAAGCAGAAAACAGAGAAACGTGAGAAATTGATCACGTATACG   737
          ||| |||     ||||| ||| || |||  ||||  |||| |||||||| |||   ||
Db  4684  TTTAGGACAATAGCCGGAGGCAGAGCAGTTGTTAAACACAGAGGTTTGAGAGCTTGTGCG  4625

Qy   738  GCATCCTGGAGGAGGAGAGCTGAAATGACCCAAGCCATCACTCGAACACAGGAGGAGA    797
          || | |||||| || | | ||    |||    ||  ||| |  ||||||||||||||||
Db  4624  CAGTGCTGAGGAGCGGCAAGGGTGAGCTGCTGCGCCCGGAGCACAAGAGGAGA   4565

Qy   798  AACTGGAACAATGTCCGAACTCTTATCACGGAGGAGTATTCCGATCATCTGGAGAAGTATCCA  857
          | ||  ||  | |||| | |  |||  ||||| |||||         ||||||||  ||||
Db  4564  AGCTCGCAGCGCCGGCCTCATCCGTCAGTATGGGACGGAGGCCTCCTCTA   4505

Qy   858  AGTTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAATGGCGCAGTTATTTCGCAG   916
          ||  |||||||| |  ||||||     || |||||   || ||| | |||| |||| | ||
Db  4504  AGCTCGTGTGGAGTCTGCCATCGAATGGCGCCGTCTGTATTTCTCCAG   4446
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RESULT 6
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pT2gpt-F1s
US-08-232-463-14

Query Match 3.2%; Score 82; DB 1; Length 7218;
Best Local Similarity 4.7%; Pred. No. 4.8e-12;
Matches 19; Conservative 244; Mismatches 139; Indels 0; Gaps 0;

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Qy   820  TATCAGGAAGTATTCCGATCACCTGGAGAACGTATCCAAGTTGGTGGAGTCAGGAATCCA   879
          ||  :::::::::::::::::::::::::::::::::::::::::::::::::: ::::::
Db  1437  TACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR  1378

Qy   880  GTTCATGGATGAGCCCGAAATGGCAGTATTTCTGCAGRATGCCAAGACCCTGTTGCAAAA   939
          :::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::
Db  1377  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR   1318

Qy   940  GATCGTGGAAGCATCAAAGGCGTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCAT   999
          :::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::::
Db  1317  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR   1258

Qy  1000  GAGCAACTTCACTGTCAATCTCAATAGAGAAGAGAAAAATTATCCGTGAAATTGACTTTC  1059
          ::::::::::::::::::::::::::::::::::::::::::::::::: ::::::: ::::
Db  1257  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR   1198

Qy  1060  TAGAGAAGAGGAGGAAGAAGAAGAAGATGCAGGAGAAATAGATGAGGAGGAAGGAGAGGA  1119
          :::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::::
Db  1197  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR   1138

Qy  1120  TGCAGTAGAAGTAGAAGAAGAGGCCAGAAAAATGTTCAAATAGCATCTTCAGGGGAAGAGGAGAG  1179
          :: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  1137  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR   1078

Qy  1180  TCTGGAGAAAGCTGCAGAGCCCTCTCAGCGTTCCCGCGAGCT   1221
          ::::::::::::     ||||||||||||||         ||||
Db  1077  RRRRRRRRRRRRRATCGGCAAGCTCCCTCGACCTGCAGCCAAGCT   1036
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RESULT 7
US-09-949-016-15195
; Sequence 15195, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 15195
; LENGTH: 4843
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15195

Query Match　　　　2.8%;　Score 73.6;　DB 4;　Length 4843;
Best Local Similarity　　67.8%;　Pred. No. 9.3e-10;
Matches 103; Conservative　0; Mismatches 49; Indels　0; Gaps　0;

Qy　765 TGACCCAAGCCATCACTCACTCGACACACAGGAGGAGGAAACTGGAACATGTCCGGAACTCTTTATCA 824
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Db　　4 TGCTGCAGGCGCCTGGCCCGGGAGCAACAGACGAAGCGTGCAGCGGGTCCGGCGCCTCATCC 63

Qy　825 GGAAGTATTCCGATCACCTGGAGAACGTATCCAAGTTGGTGGGAGTCAGGAATCCAGTTCA 884
　　　　| ||| || || | || || || ||| || |||| || || | || || ||||| ||||
Db　64 GTCAGTATGTGGGACCACCTGGAGGCCTTCCTCTAAGCTGGTGGAGTCTGCCATCCAGTCCA 123

Qy　885 TGGATGAGCCCCGAAATGGCAGTATTTCTGCAG 916
　　　　|||| |||| | | |||| ||| ||| ||||
Db　124 TGGAAGAGCCCACAAAATGGCGGCTGTATCTCCAG 155

RESULT 8
US-09-949-016-14581/c
; Sequence 14581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 14581
; LENGTH: 64309
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(64309)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14581

Query Match　　　　2.7%;　Score 71.2;　DB 4;　Length 64309;
Best Local Similarity　　61.2%;　Pred. No. 2.6e-08;

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 435
; FILING DATE:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 89149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match　　　　2.7%;　Score 69.8;　DB 1;　Length 7218;
Best Local Similarity　　2.1%;　Pred. No. 1.5e-08;
Matches　8; Conservative　235; Mismatches 132; Indels　0; Gaps　0;

Matches 115; Conservative　0; Mismatches　73; Indels　0; Gaps　0;

Qy　1009 CACTGTCAATCTCAATAGAGAGGAAGAATGAGAAGAAAATTATCCGTGAAATTGACTTTTCTAGAGAAGA 1068
　　　　|||||||||||||||||||||||||||||||||||||| |||||||||| |||||||||||| ||||||
Db　24085 CAGAGCGAAACTCCATGAAGAAGGATGAAGATGAAGATGAGATGAAGATGAAGATGATGAAGAAGA 24026

Qy　1069 GGAAGAAGGAAGAAGATGCAGGAGAAAATAGATAGATGAAGATGATGAAGGAAGAGAAGAAGATGCAGTAGA 1128
　　　　||||||||||||||| ||||||||||||||||| | |||||||| || | ||| |||| ||||| ||||
Db　24025 GGAAGAGGAAGAAGGATGCAGGAGAAGGAAGAAGAAGGAAGAAGAAGAAGAAGAAGAAGATGCAGTAGA 23966

Qy　1129 AGTAGAAGAGGCCAGAAAAATGTTCAAATAGCATCTTCAGGGGAAGAGAAGAGTCTGAA 1188
　　　　|||||| ||| ||||| ||| ||| ||||||| |||||||| ||||| ||||||||||
Db　23965 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 23906

Qy　1189 AGCTGCAG 1196
　　　　||||||||
Db　23905 AGAAGAAG 23898

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: June 15, 2005, 00:12:22 ; Search time 5372 Seconds
                                         (without alignments)
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Title: US-10-775-627A-3
Perfect score: 2590
Sequence: 1 ctcgagattacccttacag.........ctcccttccttcttcctcc 2590

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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               16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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               18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
               19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
               20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
               21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
               22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
               23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
               24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
               25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
               26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2590	100.0	2590	9	US-09-908-988B-3	Sequence 3, Appli
2	2590	100.0	2590	19	US-10-775-649-3	Sequence 3, Appli
3	2590	100.0	2590	19	US-10-775-627-3	Sequence 3, Appli
4	1266.4	48.9	1925	19	US-10-104-047-673	Sequence 673, Appl
5	910.8	35.2	2434	19	US-10-473-574-36	Sequence 36, Appl
6	910.8	35.2	2634	17	US-10-104-047-433	Sequence 433, Appl
7	910.8	35.2	2662	20	US-10-723-860-7135	Sequence 7135, Ap

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

8	899.8	34.7	1762	9	US-09-764-864-34	Sequence 34, Appl
9	485.6	18.7	2110	21	US-09-890-688-57	Sequence 57, Appl
10	461	17.8	1913	10	US-10-061-043A-20	Sequence 20, Appl
11	452	17.5	1053	15	US-10-060-6634C-20	Sequence 20, Appl
12	452	17.5	1053	17	US-10-060-6634C-20	Sequence 20, Ap
13	450.8	17.4	1431	9	US-09-908-988B-1	Sequence 1, Appli
14	450.8	17.4	1431	19	US-10-775-649-1	Sequence 1, Appli
15	450.8	17.4	1431	19	US-10-775-627-1	Sequence 1, Appli
16	440.8	17.0	2097	15	US-10-061-043A-22	Sequence 22, Appl
17	440.8	17.0	2097	17	US-10-060-6634c-22	Sequence 22, Ap
18	439.2	17.0	1764	9	US-10-094-749-1222	Sequence 1222, Ap
19	439.2	17.0	1764	18	US-10-221-625-192	Sequence 192, App
20	439.2	17.0	2700	17	US-10-723-860-7801	Sequence 7801, Ap
21	436	16.8	1781	9	US-09-764-864-21	Sequence 21, Appl
22	432.2	16.7	1597	9	US-09-908-988B-5	Sequence 5, Appli
23	432.2	16.7	1597	19	US-10-775-649-5	Sequence 5, Appli
24	432.2	16.7	1597	19	US-10-775-627-5	Sequence 5, Appli
25	419.4	16.2	867	15	US-10-061-043A-38	Sequence 38, Appli
26	419.4	16.2	867	17	US-10-060-6634c-38	Sequence 38, Appl
27	373.6	14.4	587	9	US-09-764-864-493	Sequence 493, App
28	308.6	11.9	2040	18	US-10-250-613-22	Sequence 22, Appl
29	288.2	11.1	630	15	US-10-061-043A-32	Sequence 32, Appl
30	288.2	11.1	630	17	US-10-060-6634C-32	Sequence 32, Appl
31	285.2	11.0	630	9	US-09-918-995-32020	Sequence 32020, A
32	243.8	9.4	496	10	US-09-918-995-2958	Sequence 2958, Ap
33	241.8	9.3	531	11	US-09-864-408A-6101	Sequence 6101, Ap
34	167	6.4	424	10	US-09-918-995-5316	Sequence 5316, Ap
35	156.6	6.0	411	10	US-09-918-995-4809	Sequence 4809, Ap
36	151	5.8	446	9	US-09-764-864-482	Sequence 482, App
37	149.8	5.8	638	17	US-10-191-803-895	Sequence 895, App
38	140.4	5.4	1039	9	US-10-880-192-25	Sequence 25, Appl
39	140.4	5.4	1039	16	US-10-427-348-25	Sequence 25, Appl
40	133.8	5.2	766	20	US-10-723-860-7957	Sequence 7957, Ap
41	133.8	5.2	2000	14	US-10-199-846-10290	Sequence 10290, A
42	114.2	4.4	475	20	US-10-723-860-4075	Sequence 4075, Ap
43	73.6	2.8	424	10	US-09-918-995-4490	Sequence 4490, Ap
44	72	2.8	3127	17	US-10-110-260A-1109	Sequence 1109, Ap
45	71	2.7	31124	13	US-10-087-192-463	Sequence 463, App

ALIGNMENTS

RESULT 1
US-09-908-988B-3

; Sequence 3, Application US/09908988B
; Patent No. US20020127690A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG.028US
; CURRENT APPLICATION NUMBER: US/09/908,988B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1714)
US-09-908-988B-3

Query Match   100.0%; Score 2590; DB 9; Length 2590;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2590; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CTCGAGATTACCCTTACAGAAGCTGTTCGGGAGCACCTTTCCTTGGCAGCACACTCAG 60

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Db          1 CTCGAGATTTACCCTTACAGAAGCTGTTCGGGAGCACCTTTCCCTTGGCAGCACACTCAG 60

Qy         61 GGACAGGGACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGACAGGGACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCA 120

Qy        121 GCAGACCATGGATAACTTGGAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGACCATGGATAACTTGGAAAAGCAACTGATCTGTCCCATCTGCCTAGAGATGTTCAC 180

Qy        181 GAAGCCTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGCCTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCAGGAAATGTGCCAGTGACAT 240

Qy        241 CTTCCAGGCCTCTAACCCGTACTTACCCACAAGAGGAGGCACCACCGTGGCATCAGGGGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTTCCAGGCCTCTAACCCGTACTTACCCACAAGAGGAGGCACCACCGTGGCATCAGGGGG 300

Qy        301 CCGCTTCCGCTGTCCCTCCTGCAGACATGAGGTGGTGTTAGACAGACATGGGGTCTATGG 360
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Db        301 CCGCTTCCGCTGTCCCTCCTGCAGACATGAGGTGGTGTTAGACAGACATGGGGTCTATGG 360

Qy        361 ACTGCAGAGGAACCTGCTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTGCAGAGGAACCTGCTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCCACCAG 420

Qy        421 GCCAGAAAAAAAAATTGGACCAGCCCATGTGTGAAGAGCATGAAGAGGAACGCATCAACAT 480
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Db        421 GCCAGAAAAAAAAATTGGACCAGCCCATGTGTGAAGAGCATGAAGAGGAACGCATCAACAT 480

Qy        481 CTATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAA 540
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Db        481 CTATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTGCAAGGTTTTTGGCGCCCATAA 540

Qy        541 GGACTGCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGCAGAAGTCAGAGCTCAGTGA 600
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Db        541 GGACTGCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGGCAGAAGTCAGAGCTCAGTGA 600

Qy        601 TGGTATTGCTGTACTTGTGGGAAGCAACGATAGAGTCCAGGGTGTGATCAGCCAGCTGGA 660
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Db        601 TGGTATTGCTGTACTTGTGGGAAGCAACGATAGAGTCCAGGGTGTGATCAGCCAGCTGGA 660

Qy        661 GGACACCTGTAAAACTATTGAGGAGTGCTGCAGAAAGCAGAAACAGGACCTGTGTGAGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGACACCTGTAAAACTATTGAGGAGTGCTGCAGAAAGCAGAAACAGGACCTGTGTGAGAA 720

Qy        721 ATTTGATCACCTATACGGCATCCTGGAGGAGAGGAAGACTGAAATGACCCAAGCCATCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTGATCACCTATACGGCATCCTGGAGGAGAGGAAGACTGAAATGACCCAAGCCATCAC 780

Qy        781 TCGAACACAGGAGGAGAAACTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCGAACACAGGAGGAGAAACTGGAACATGTCCGAACTCTTATCAGGAAGTATTCCGATCA 840

Qy        841 CCTGGAGAACGTATCCAAGTTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCTGGAGAACGTATCCAAGTTGGTGGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAAT 900

Qy        901 GGCAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGC 960
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Db        901 GGCAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGATCGTGGAAGCATCAAAGGC 960

Qy        961 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGCAACTTCACTGTCAATCT 1020

Qy       1021 CAATAGAGAAGAAAAAATTATCCGTGAAATTGACTTTTCTAGAGAAGAGGAAGAGGAAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAATAGAGAAGAAAAAATTATCCGTGAAATTGACTTTTCTAGAGAAGAGGAAGAGGAAGA 1080

Qy       1081 AGATGCAGGAGAAATAGATGAAGAAGGAGAAGGAGAGGATGCAGTAGAAGTAGAAGAGGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGATGCAGGAGAAATAGATGAAGAAGGAGAAGGAGAGGATGCAGTAGAAGTAGAAGAGGC 1140

Qy       1141 AGAAAATGTTCAAATAGCATCTTCAGGGGAAGAGGAGAGTCTGGAGAAAGCTGCAGAGCC 1200
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Db       1141 AGAAAATGTTCAAATAGCATCTTCAGGGGAAGAGGAGAGTCTGGAGAAAGCTGCAGAGCC 1200

Qy       1201 CTCTCAGCTTCCCGCAGAGCTTCAGGTCGCCCCAGAGCCACTACCTGCTTCCTCTCCAGA 1260
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Db       1201 CTCTCAGCTTCCCGCAGAGCTTCAGGTCGCCCCAGAGCCACTACCTGCTTCCTCTCCAGA 1260

Qy       1261 ACCGTTTTCATCCATGCCACCTGCTGCAGATGTCCTGGTGACACAGGGGGAGGTGGTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ACCGTTTTCATCCATGCCACCTGCTGCAGATGTCCTGGTGACACAGGGGGAGGTGGTGCC 1320

Qy       1321 CATTGGCTCTCAGCAGACCACACAGTCTGAAACTTCAGGCCCTTCAGCAGCGGAAACTGC 1380
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Db       1321 CATTGGCTCTCAGCAGACCACACAGTCTGAAACTTCAGGCCCTTCAGCAGCGGAAACTGC 1380

Qy       1381 GGATCCCTTGTTTTACCCTAGTTGGTATAAAGGCCAAAGCCGGAAAACCAGCTCCAACCC 1440
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Db       1381 GGATCCCTTGTTTTACCCTAGTTGGTATAAAGGCCAAAGCCGGAAAACCAGCTCCAACCC 1440

Qy       1441 ACCTTGCACTCATGGAGTGAAGGTCTGGGTCAAATAGGGCCTCTGGGCATTGAGGATTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACCTTGCACTCATGGAGTGAAGGTCTGGGTCAAATAGGGCCTCTGGGCATTGAGGATTC 1500

Qy       1501 CAGTGTGCAGTCCGCAGAAGTGGCAGAAGCCGCAACCAATGAGCAGGCAGCAGTGAGTGG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CAGTGTGCAGTCCGCAGAAGTGGCAGAAGCCGCAACCAATGAGCAGGCAGCAGTGAGTGG 1560

Qy       1561 TAAGGAGTCTAGTTCAACTGCAGCTACCTCTCAGATTGGATTTGAGGCCCCTTCTCCCCA 1620
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Db       1561 TAAGGAGTCTAGTTCAACTGCAGCTACCTCTCAGATTGGATTTGAGGCCCCTTCTCCCCA 1620

Qy       1621 GGGACAGTCTGCAGCCTTGGGGAGTGGGGGTGGGGTGATCCTGAGCCAGCTCGCCACGTC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGGACAGTCTGCAGCCTTGGGGAGTGGGGGTGGGGTGATCCTGAGCCAGCTCGCCACGTC 1680

Qy       1681 TTCTCCTTCTCCTGGTTTGAATTCCCTAAATGAATAATATTTATTCTCGTTGCTGCCCCC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TTCTCCTTCTCCTGGTTTGAATTCCCTAAATGAATAATATTTATTCTCGTTGCTGCCCCC 1740

Qy       1741 TGTCTGCCTGGCTGAAAAGCACATAGGCAGCAGGAAACAGGTGGAAATTCACCACGATTC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGTCTGCCTGGCTGAAAAGCACATAGGCAGCAGGAAACAGGTGGAAATTCACCACGATTC 1800

Qy       1801 ATATGAAGGGGACCTCTGGACAGGATTTCTGAAAGCAAAACAAAACAATACAACACCACC 1860
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Db       1801 ATATGAAGGGGACCTCTGGACAGGATTTCTGAAAGCAAAACAAAACAATACAACACCACC 1860

Qy       1861 ACCCTTTAATTCCAGATGACTTATCTCACTCATTGAGAAAATGATTATGCTCAGAACAAA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 ACCCTTTAATTCCAGATGACTTATCTCACTCATTGAGAAAATGATTATGCTCAGAACAAA 1920

Qy       1921 ATTACAGAAAATACTCTTCTGAAGAAACTTGATCTTCTGCAAATCTTTCATTTGTGTGAG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 ATTACAGAAAATACTCTTCTGAAGAAACTTGATCTTCTGCAAATCTTTCATTTGTGTGAG 1980

Qy       1981 AAACCTTCTGAAGGTTGTGTAGGTGTGGTGCATGCCTGTGTATCAGCCATAAGTGCCAAG 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AAACCTTCTGAAGGTTGTGTAGGTGTGGTGCATGCCTGTGTATCAGCCATAAGTGCCAAG 2040

Qy       2041 TGGTAACAAAGTGGCAGAACACTCTCCCAGCCTCCCTCAGGCTTCTGGTTATTTAGGAC 2100
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Db       2041 TGGTAACAAAGTGGCAGAACACTCTCCCAGCCTCCCTCAGGCTTCTGGTTATTTAGGAC 2100

Qy       2101 GCTTGTGCCTTTTGCTTTTCTCCTTAGCATTGCAGGTGGTAGGTGATGTTCAGTGTCAGT 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCTTGTGCCTTTTGCTTTTCTCCTTAGCATTGCAGGTGGTAGGTGATGTTCAGTGTCAGT 2160

Qy       2161 TCCAAACTGACCGATTTATCAAAATATGGAGATTGGTCACTGACCAAAGCTATGTAGGGC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TCCAAACTGACCGATTTATCAAAATATGGAGATTGGTCACTGACCAAAGCTATGTAGGGC 2220
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RESULT 2
US-10-775-649-3
Sequence 3, Application US/10775649
Publication No. US20040132160A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028USD2
CURRENT APPLICATION NUMBER: US/10/775,649
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 09/908,988
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/219,020
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3
LENGTH: 2590
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (80)...(1714)
US-10-775-649-3

Query Match 100.0%;   Score 2590;   DB 19;   Length 2590;
Best Local Similarity 100.0%;
Matches 2590;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
Pred. No. 0;

[Nucleotide sequence alignment (Qy/Db) follows, with paired query (Qy) and database (Db) rows numbered in increments of 60 and 120 respectively, spanning positions 1–2590.]

RESULT 3
US-10-775-627-3

; Sequence 3, Application US/10775627
; Publication No. US20040142446A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: SPENCER, JEFFREY A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
; TITLE OF INVENTION: AND INTERMEDIATE FILAMENTS IN STRIATED MUSCLE CELLS
; FILE REFERENCE: MYOG:028USD1
; CURRENT APPLICATION NUMBER: US/10/775,627
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 09/908,988
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,020
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1714)
US-10-775-627-3

Query Match 100.0%; Score 2590; DB 19; Length 2590;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CTCGAGATTTACCCTTACAGAAGCTGTTCGGGAGCACCTTTCCCTTGGCAGCACACTCAG 60
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Db   1 CTCGAGATTTACCCTTACAGAAGCTGTTCGGGAGCACCTTTCCCTTGGCAGCACACTCAG 60

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Qy   361 ACTGCAGAGGAGGAACCTGCTCGTGGGAAAAACATTATTAGTGATATCTACACAGCAGGAATCCACCAG  420
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Db   361 ACTGCAGAGGAGGAACCTGCTCGTGGGAAAAACATTATTAGTGATATCTACACAGCAGGAATCCACCAG  420

Qy   421 GCCAGAGAAAAAAATTGGACCAGCCCATGTGTGTGAAGAGCATGAAGACGCATCAACAT           480
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Db   421 GCCAGAGAAAAAAATTGGACCAGCCCATGTGTGTGAAGAGCATGAAGACGCATCAACAT           480

Qy   481 CTATTGTCTGAACTGTGAAGTGCCCACCACTGTTCCTTGTTGTCGAAGTTTTTGGGCCCCATAA       540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CTATTGTCTGAACTGTGCCCACCACCGTTCCTTGTCGTCAAGGTTTTTGCGGCCCATAA           540

Qy   541 GGACTGCCAGGTGGCTCCCCCTGACTCATGTGTTCCAGAGGGCAGAGACTTCAGTGA            600
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Db   541 GGACTGCCAGGTGGCTCCCCCTGACTCATGTGTTCCAGAGGGCAGAGACTTCAGTGA            600

Qy   601 TGGGTATTTGCTACTTGTGGGAAGGCAACCATGTCCAGGGTGTGATCAGCCAGCTGGA           660
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Db   601 TGGGTATTTGCTACTTGTGGGAAGGCAACCATGTCCAGGGTGTGATCAGCCAGCTGGA           660

Qy   661 GGACACACCTGTAAAAACTATTGACGAGTGCTGCAGAAAACAGGACCCTGTGTGTGAGAA         720
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Db   661 GGACACCCTGTAAAAACTATTGACGAGTGCTGCAGAAAACAGGACCCTGTGTGTGAGAA          720

Qy   721 ATTTGATCACCTATACGGCCATCCTGGAGGAGGAGGACTGAAATGACCCAAGCCATCAC         780
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Db   721 ATTTGATCACCTATACGGCCATCCTGGAGGAGGAGGACTGAAATGACCCAAGCCATCAC         780

Qy   781 TCGAACACAGGAGGAGAAACTGGACACATGTCCGAACTCTTTATCAGGAGGAAGTATTCCGATCA      840
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Db   781 TCGAACACAGGAGGAGAAACTGGACACATGTCCGAACTCTTTATCAGGAGGAAGTATTCCGATCA      840

Qy   841 CCTCGGAGAACGTATCCAAGTTGGTGGAGTCAGTCAGTTCATGGAGCCCGAAAT             900
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Db   841 CCTCGGAGAACGTATCCAAGTTGGTGGAGTCAGTCAGTTCATGGAGCCCGAAAT             900

Qy   901 GGCAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAGATCGTGGAAGCCATCAAAAGGC        960
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Db   901 GGCAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAGATCGTGGAAGCCATCAAAAGGC        960

Qy   961 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGACAACTTCACTGTCAATCT        1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GTTTCAGATGGAGAAACTAGAACAAGGTTATGAGATCATGAGACAACTTCACTGTCAATCT        1020

Qy  1021 CAATAGAGAAGAAGAAAAAATTATCCGTGAAATTGACTTTTCTAGAGAAGAAGAGGAAGA         1080
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Db  1021 CAATAGAGAAGAAGAAAAAATTATCCGTGAAATTGACTTTTCTAGAGAAGAAGAGGAAGA         1080

Qy  1081 AGATGCAGGAGAAAATAGATGAAGAAGGAGATGCAGTAGAAGTAGAAGAAGGC              1140
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Db  1081 AGATGCAGGAGAAAATAGATGAAGAAGGAGATGCAGTAGAAGTAGAAGAAGGC              1140

Qy  1141 AGAAAATGTTCAAATAGCATCTTCAGGGAGAGAGTCTGGAGAAGAAAGCTGCAGAGCC           1200
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Db  1141 AGAAAATGTTCAAATAGCATCTTCAGGGAGAGAGTCTGGAGAAGAAAGCTGCAGAGCC           1200

Qy  1201 CTCTCAGCTTCCCGCGAGAGCTTCAGGTCGCCCCAGAGCCACTACCTGCTTCCTCTCCAGA        1260
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Db  1201 CTCTCAGCTTCCCGCGAGAGCTTCAGGTCGCCCCAGAGCCACTACCTGCTTCCTCTCCAGA        1260

Qy  1261 ACCGTTTCATCCATGCCACCTGCTGCAGAGTCCTGGTCAGTGACACAGGGTGGTGCC           1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ACCGTTTCATCCATGCCACCTGCTGCAGAGTCCTGGTCAGTGACACAGGGTGGTGCC           1320

Qy  1321 CATTGGGCTCTCAGCAGACCACACACCTGCCGGGCCCTTCAGCAGGGGGAAAACTGC           1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 CATTGGGCTCTCAGCAGACCACACACCTGCCGGGCCCTTCAGCAGGGGGAAAACTGC           1380

Qy  1381 GGATCCCTTGTTTTTACCCTAGTTGGTGTATAAAGGGCCAAAGCCGGAAAACCAGCTCCAAACCC     1440
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Db  1381 GGATCCCTTGTTTTTACCCTAGTTGGTGTATAAAGGGCCAAAGCCGGAAAACCAGCTCCAAACCC     1440


Qy  1441 ACCTTGCACTCATGGGAGTGAAGTTCTGGGTTCAAATAGGGCCCTGGGTCATTGAGGATTC       1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 ACCTTGCACTCATGGGAGTGAAGTTCTGGGTCAAATAGGGCCCTGGGTCATTGAGGATTC       1500

Qy  1501 CAGTGTGCAGTCCGCAGAGTGGGCAGAAGTGGCAGAAGCCGCAACCAATGAGCAGTGAGTGG      1560
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Db  1501 CAGTGTGCAGTCCGCAGAGTGGGCAGAAGTGGCAGAAGCCGCAACCAATGAGCAGTGAGTGG      1560

Qy  1561 TAAGGAGTCTAGTTCAACTGCAGCTTACCTCTCAGATTGGATTGAGGGCCCTTTCTCCCCA       1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TAAGGAGTCTTAGTTCAACTGCAGCTTACCTCTCAGATTGGATTGAGGGCCCTTTCTCCCA       1620

Qy  1621 GGGACAGCAGTCTTGCAGCCCTTGGGGGACTGGGGGTGGGGGGGTCCTGGCCAGCTCGCACGTC      1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 GGGACAGTCTTGCACGCCTTGGGGACTGGGGGTGGGGGGTGATCCTGGCCAGCTCGCACGTC       1680

Qy  1681 TTCTCCTTCTCCTGGTTTGAATTCCCTAAATGAATAATGAATAATATTATTCTGGTTGCTTGCCC     1740
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Db  1681 TTCTCCTTCTCCTGGTTTGAATTCCCTAAATGAATAATGAATAATATTATTCTGGTTGCTTGCCC     1740

Qy  1741 TGTCTGCCTGGCTGAAAAGCCACATAGGCGAGCAGGAAACACAGTGGGAAATTCACCAGGATTC      1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTCTGCCTGGCTGAAAAGCCACATAGGCGAGCAGGAAACACAGTGGGAAATTCACCAGGATTC      1800

Qy  1801 ATATGAAAGGGGACCCTCTGGACAGGGATTTCTGAAAAGCAAAACAATACAACAACACCACC       1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 ATATGGAAGGGGACCCTCTGGACAGGGATTTCTGAAAAGCAAAACAATACAACAACACCACC       1860

Qy  1861 ACCCTTTAATTCCAGATGACTTATCTCACTCATTGAGAAAAGATGATTATGGTCAGAACAA        1920
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Db  1861 ACCCTTTAATTCCAGATGACTTATCTCACTCATTGAGAAAAGATGATTATGGTCAGAACAA        1920

Qy  1921 ATTACAGAAAATACTCTTCTGAAGAAGACTTGATCTTCTGCAAAATCTTTCATTTGTGTGAG       1980
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Db  1921 ATTACAGAAAATACTCTTCTGAAGAAGACTTGATCTTCTGCAAAATCTTTCATTTGTGTGAG       1980

Qy  1981 AAAACCTTCTGAAAGGTTGTGTGTTAGTGGTGGTGTGTATCAGCCATAAGTCCAAG           2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 AAAACCTTCTGAAAGGTTGTGTGTTAGTGGTGGTGTGTATCAGCCATAAGTCCAAG           2040

Qy  2041 TGGTAACAAAGTGGCAGAACACTCTCCCAGCCTCCCTCAGGCTTCTTGGTTATTTTAGGAC        2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TGGTAACAAAGTGGCAGAACACTCTCCCAGCCTCCCTCAGGCTTCTTGGTTATTTTAGGAC        2100

Qy  2101 GCTTGTGCCCTTTTGCTTTTCTCCTTAGCATTGCAGTGGTAGGTGTGGTTCAGTCAGT         2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 GCTTGTGCCTTTTGCTTTTCTCCTTAGCATTGCAGTGGTGATTGTTGTCAGTCAGT          2160

Qy  2161 TCCAAAACTGACCGGATTTATCAAAAATATGAGAGATTGGTCACTGACCAAAGCTATGTGTAGGGC    2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 TCCAAAACTGACCGATTTATCAAAAATATGGAGATTGGTCACTGACCAAAGCTATGTAGGGC       2220

Qy  2221 ACTGTAGAGGTTCCTTTCCCTTATGGAATGCCATGGGGTGCGAGACAGGACTTCCTTACA        2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 ACTGTAGAGGTTCCTTTCCCTTATGGAATGCCATGGGTGCGAGACAGGACTTCCTTACA         2280

Qy  2281 TGTGGCCACACGTCCATAGTGCCAGAAGGCCAAAAATTCTAGGGCAACTCTTTTGACATTTT      2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 TGTGGCCACACGTCCATAGTGCCAGAAGGCCAAAAATTCTAGGGCAACTCTTTTGACATTTT      2340

Qy  2341 TCTAACCTTATTTACATAGTCTCATAATCATATCCAGTGTTGATTAATCTGATTAATCTGTG       2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TCTAACCTTATTTACATAGTCTCATAATCATATCCAGTGTTGATTAATCTGATTAATCTGTG       2400

Qy  2401 CAAAGAGGAGCTGTCTACTTTCTTAAGTAGTCCTGCCATAGCGACAGCAATCTGATAAATCTGTG     2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 CAAAGAGGAGCTGTCTACTTTCTTAAGTAGTCCTGCCATAGCGACAGCAATCTGATAAATCTGTG     2460

Qy  2461 CATTGGGCTCTCAGCAGACCACACAGTTGTACTTTTCTTAAGTGTATACACACAAATTCTCCCCGTC    2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GAGCAACTGCATGGATTTAAGTAGTATACACACAAATTCTCCCCGTGTGTCCCTGTGTCTCTC      2520

Qy  2521 TCTCTCTCCCCTCTCCTGTCTTCTCCCCCTCTCCCCTCTCCTGTTCTCCCTCCTTTCCT         2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TCTCTCTCCCCTCTCCTGTCTTCTCCCCCTCTCCCCTCTCCTGTTCTCCCTCCTTTCCT         2580
```

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Db   2521 TCTCTCTCCCCCCTCTCTCCCTCCTGTCTCTCTCTCTCCCCCTCCCTGTCTCTCTCCCCCCTTTCCT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2581 TTCTTCCTCC 2590
          ||||||||||
Db   2581 TTCTTCCTCC 2590
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RESULT 4
US-10-104-673

Sequence 673, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: HI-A0105
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: No. US20030236392A1e1 full length cDNA
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 673
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-673

Query Match   48.9%;   Score 1266.4;   DB 17;   Length 1925;
Best Local Similarity   82.0%;   Pred. No. 0;
Matches 1571;   Conservative   0;   Mismatches 301;   Indels 44;   Gaps 8;

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Qy    66 GGGGACAGCCGGCAAGGAAAATGAGACACTTCTCTGAATTACTACAAGTCTTTCTTCCAAAAGAGCAGCAGGAGA 125
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    33 GGGGACAGGGAGGAGGATGAGCGCCATCTCTGAATTACAAAATCTTTTTCCAAAGAGCAGCAGA 92

Qy   126 CCATGGGATAACTTGGGAAAAGCAAACTGGACTCGTGTCCCATCTGCCTAGAGATGTTCACGAAGC 185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    93 CCATGGGATAACTTAGGAGAAGCAAACTCATCTGCTTCAAGAGATGTTCACGAAAC 152

Qy   186 CTGTGGTCATTCTCCCTTGCCAGCACAAACCTGTCGCAGGAAAATGTGCGACCATCTTCC 245
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   153 CTGTGGTGATTCTCCCTTGTCAGCACAAACCTGTGTAGGAAAATGTGCCAGTGATGTATTTTCC 212

Qy   246 AGGCCTCTTAACCCGTACTTACCCACCACAAGAGGAGCGACCACCACCGTGGGCATCACGGGGCGGCT 305
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   213 AGGCCTCTTAACCCGTATTTGCCCACAAGAGGGTCACCATGGCCATCACGGGGCCGAT 272

Qy   306 TCCGCTGTCCCTTCCTGCGAGACATGAGAGGTGGTGGGTCTCTATGGACTGGC 365
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   273 TCCGGCTGCCCCATCCTGTAGACATGAAGTGGGTTTTTGGATAGAACATGGGCGTATATGGGACTTC 332

Qy   366 AGAGGAACCTGCTCGTCGTGGAAAACATTATTGATATCTACACAGGCAGCAG 425
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   333 AGAGGAACCTGCTGGTGGAAAATATCATTGACATCTACACCAGGCCAG 392

Qy   426 AAAAAAAAATTGGACCAGCCCATGTGTGAAGAGCATGAAGGGAACCCATCAACACATCTATT 485
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393 AAAAGAAAATCCGACACCAGCCCATGTGCGAGAACAATGAGAGAGCGCCATCAACATCTACT 452

Qy   486 GTCTGAACTGTGAAGTGCCCACCCGTTCCTTGTGCAAGGTTCCATGAACGACT 545
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   453 GTCTGAACTCGGAAGTACCCACCCGTGTTGGTGCAAGGTTTTGGTCACACAAGACT 512

Qy   546 GCCAGGTGGCTCCCCTGACTCACTCATGTGTTCCAGGGCCAGAGGTCAGTAGTGGTA 605
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   513 GCCAGGTGGCTCCCCTCACTCATGTGTTCCAGGGCCAGAGCTCAGTGATGGCA 572

Qy   606 TTGCTCGTACTTGTGTGGGAAGCAACGATAGAGTCCAGGAGTAGAGGCACA 665
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   573 TCGCCATCCTCGTGGGCGCAACGATCGAGTGGATCAGGCAGTGGGAAGACA 632

Qy   666 CCTGTAAACTATTGAGGAGTGCTGCAGAAAAGCAGAAAACAGGACCTCGTGTGAGAAAATTTG 725
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 CCTGTAAACTATTGAGGAGTGCTGCAGAAAAGCAGAAAACAGGACCTCGTGTGAGAAAATTTG 725
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Db   633 CCTGCAAAACTATCGAGGAATGTTGCAGAAAATGACTGAAAATCATCACTTGG 692
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   726 ATCACCTTATACGGGCATCCTGGAGGAGAACTGAAATGACCAAGCACTCGAA 785

Db   693 ATTACCTGTATGGCATTTTGGAGGAGGAGAAGTGCCAAGTCATTACCCGA 752
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   786 CACAGGAGGAGAAAACTGGACACATGTCCGACACTCTTATCAGGAACTCACCTGG 845

Db   753 CCCAAGAGGAGAAACTGGAACACATGTCCGTGCCTCTGAATCAAAAGTATTCTGATCATTGG 812
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   846 AGAACGTATCCAAGTTGGTGGAGTGCCAGAATCCAGTTCAGTGGCCAGAAATGGCAG 905

Db   813 AGAACGTTCTCAAAGTTGGTTGAGTGGCAGGAATTCAGTTTATCGGATGAGCCAGAAATGGCAG 872
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   906 TATTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGGGCGTTTC 965

Db   873 TGTTTTCTGCAGAATGCCAAAAACCCTGCTAAAAAAATCTCGGAAGCCATCAAAAGGGCATTTC 932
         ||||||||||||||||||||||||||||||||||||||||||
Qy   966 AGATGGAGGAAACTAGAACAGTTTATGAGATCATGAGCAACTTCACTGTCAATCTCAATA 1025

Db   933 AGATGGAGAAAAATAGAACATGGCTATGAGAAACATGAAACCACTTCACAGTCAACCTCAATA 992
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1026 GAGAGAGAAAATAGAATGAAGAAGGAAGGAGAA------------GGATGCAGTAGAAG 1130

Db   993 GAGAGAGAAAAGTAAATACGTGAAAAATTGACTTTTTACAGAAGATGAAGATGAAGAAGATG 1052
         ||||||||||||||||||||||||||||||||||||||||
Qy  1086 CAGGAGAAAATAGGATGAAGAAGGAAGGAGGAGGA------------GGATGCAGTAGAAG 1130

Db  1053 AAGAAGGCGGAGAAGAGGAAGGAGAAGAAGAAGGAGGAGGAGAAGTGGAGGAAGCAGTAGAAG 1112
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1131 TAGAAGAGGGCAGGAAAATGTTCAAGAAGACTTTCAGGGAAGGAGATGAAGAGTCTGGGGAAAG 1190

Db  1113 TGGGAAGAGAGGTAGAAAATGTTCAAGACAGAGTTTCCAGGAGAAGATGAAAACCCAGAGAAAAAG 1172

Qy  1191 CTGCAGAGCGCCCTCTCAGCTTCCCGGAGCTTCAGTGTCGCCCGAGAGCCACTACCTGCTT 1250

Db  1173 CTTCAGAGCTCTCTCAG------GTGGAGCTGCAGGCGTCGGCCCTGGGCACTTCCAGTTT 1226

Qy  1251 CCTCTCCAGAACCGTTTTCATCCAAGCCACCTGCTGCAGATGTCGGAGATGTCGACAGGGGG 1310

Db  1227 CCTCTCCAGAGCGGCCACCTCCAGCCTGCCACCTGTGTCGGATGTCGCCCTGTGCAGAGGGGG 1286

Qy  1311 AGGTGGTTGCCCATTGGCTGCTGCAGCAGAAACAGCACAGTGGGGAAACTTCAGCGGCAG 1370

Db  1287 AGGTTGTTGTACCCACGGGGCTTCTGAGCGAGCACCACAGAAGTCCAGTCCCCTGCAGCAG 1346

Qy  1371 CGGGAAACTGCGGGAATCCCCTGGTTGTTTTCCCTGGGTGGTTGGTTATAAAGGCGGAAAACCA 1430

Db  1347 CAGAAAACTGGCGAACCCTTGTTTTTACCCTAGTTGGTTATAAAGGCCAAAACCCGAAAGCCA 1406

Qy  1431 GCTCCAACCCACCTTGCACTCATGGGAGTGGAAGGTGAAGGTCAGTGTGGGCCTCTGGGCA 1490

Db  1407 CCACCAAACCCACCTTGCACCCCAGGAGTGCAAGGTGGGCGCAAAGGACCTCCAGGTT 1466

Qy  1491 TTGAGGAGTTCCAGTGTGTCGCGCAGAAGGTGCGAGAAGCCCCACCAATGACGAGCGCAG 1550

Db  1467 CTGAGGAGTTCGAAGTTGTACCGGAAGGCAGAAGTGGCAGCAGCGAGTGAGAAGCGGCAG 1526

Qy  1551 CAGTGAGGTGGTTGAAGGAGTCTCAGTTCAACCTTCAGCGTACCTCTCAGATTGGAGGCCC 1610

Db  1527 CTGTGAGCTGGGTTAAGGGAAAACTAGTGCACCGTCTTTCTCAGATTGGATTGGAGGCTC 1586

Qy  1611 CTTCTCCCCAGGGACAGTCTGCAGCCTTTGGGGAGGTCGGTGGG--GGTGAATCCTGAGCCC 1669

Db  1587 CTCCCCTTCCAGGGACCAGGCTTCCAGCGTTCCAGGCAGTGGAGTCGGCCAG 1646

Qy  1670 CTCCGCCACGTCTTCTTCCTGTTTGAATTCCCTAAATGAATTAATAATTATTCTCG 1729

Db  1647 CTCGCCATATCTTCTTCCTTTTCCTGG--TTGAACTCCCTAAATGAATGAATATTCCAA 1705

Qy  1730 TTGCTGCCCC--CTGTCTGCCTTGGCTGAAAAGCACAATAGGCAGCAGAAACAGGTGGAAAT 1788

Db  1730 |||||||||||                                      ||
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Db   1706  CTGCTGCCCTCTCGTCTGCTGGCTGGATGGCATGTGGGCAGCAGGAGCGAAGCCCAAGTGAA
Qy   1789  TCACCACGATTCA---TATGAAGGGGAGCCTCTGGGACAGGAGTTTCTGAAAGCAAAACAAA  1845
Db   1766  TTAATATTATGCAGATGAATAAAGGGGACCTTCTGAACAGGAGATTTCTTCGCA-------  1813
Qy   1846  CAATACACACCACCACCCTTTAATTCAGATGACTTATCTCAC-TCATTGAGAAAATGA  1904
Db   1814  ----AAAATAGGCCCCAAAACTGCAATTCCATATGACTTATCTCAACATCTTGGGGTGGGAAAGA  1869
Qy   1905  TTATGCTCAGAACAAAATTACAGAAAAATACTTCTTCTGAAGAAAACTTGATCTTCTCC  1960
Db   1870  ATATTTTTGAGAAAATAGTTGCAGAAAGCACTCGGGAAATAATAAACTTGATCTTATAC  1925
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Qy     66  GGGACACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGA   125
           ||||| |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    170  GGGACAGCAGCGAGGAGGATGAGCGGCCATCTCTGAATTACAAATCTTTTCTCCAAAGAGCAGCAGA   229

Qy    126  CCATGGATAACTTGAAAAAGCAACTGATCTGTGTCCCATCTGCCTAGAGATGTTCACGAAGC   185
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230  CCATGGATAACTTAGAAAAGCAACTCATCTGTGTCCCATCTGCCTAGAGATGTTCACGAAAC   289

Qy    186  CTGTGGGTCATTCTCCCTTGCCAGCACAACCTGTCAGGAAGGGAAAGTGCCAGTGAACATCTTCC   245
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    290  CTGTGGGTGATTCTCCCTTGTCAGCACAACCTGTGTAGGAAGGGAAAGTGTGCCAGTGATATTTTCC   349

Qy    246  AGGCCTTCTAACCCGTTACTTACCCACAAGAGGCACCACCGTGGCATCAGGGGCGCGCT   305
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    350  AGGCCTTCTAACCCGTTATTTGCCCACACAAGAGGGTACCACCATGGCATCAGGGGCGGAT   409

Qy    306  TCCGCTGGTCTCCCTCCTGCAGACATGAAGGTGGTTGGTAGGACGACATGGGGTCTTATGGACTGC   365
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410  TCCGCTGCCCATCCTGTAGGACATGAAGGTGTTTTGGATAGACATGGGGGTATATGGACTTC   469

Qy    366  AGAGGAACCTGCTCGTGTGGGAAAACATTATTATCTACAAGCAGGAGAATCCACCAGGCCAG   425
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    470  AGAGGAACCTGCTCGTGTGGGAAAATATCATTGACAATCTACAAGCAGGAGAGTCCAACCAGGCCAG   529

Qy    426  AAAAAAAAATTGGACCAGCCCCATGTGTGAGAGCATGAAGGAAGCGCATCAAACATCTATT   485
           ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530  AAAAGAAATCCGACCAGCCCATGTGCGAGGAACATGAAGGAGGCGCATCAAACATCTACT   589

Qy    486  GTCTGAACTGTGAAGTGCCCACCCGTTCCTTGTGCAAGGTTTTGCGCGCCCATAAGGACT   545
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    590  GTCTGAACTGCGAAGTACCCACCCGTCCTCTGTGCAAGGGTGTTTTGGTGCACAAAAGACT   649

Qy    546  GCCAGGTGGCTCCCCTGACTCATGTGTTCCAGAGCCAGAAGTCCAGTGATGATGGTA   605
           ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    650  GCCAGGTGGCTGCTCCCCACTCACTGTGTTCCAGAGACAGAAGTCTCAGTGATGATGGCA   709

Qy    606  TTGCGTGACTTGTTGGGAAGCAAACGATAGAGTCTCCAGGGTGTTGGGTGCAGGAGGACA   665
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    710  TCGCCAATCCTCGTGGGCAGCAAACGATCCGAGTCTCCAGGGTGTTGGGTGCAGGAGACA   769

Qy    666  CCTGTAAAACTATTGAGGAGTGCTCGCAGAAAAGCCAGAGAAACAGGACTTGTGTGAGAAATTG   725
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    770  CCTGCAAAACTATCGAGGAATGTTCGCAGAAACAGAAAACAAGAGCTTTTGTGTGAGAGTTTG   829

Qy    726  ATCACCTATACGGCATCCTGGAGGAGGACTGAAATGACCCAAAGCACTCACTCGAA   785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    830  ATTACCTGTACGGCATTTTGGAGGAGGAGAATGAAATGACCCAAAGTCATTACCCGAA   889

Qy    786  CACAGGAGGAGGAAACTGGAACATGTCCGGAACTCTTATCAGCGGATCACCTGG   845
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    890  CCCAGAGGAGAAAACTGGAACATGTCCGTGCTCTGACTCAAAAGGATTCTCATCATTGG   949

Qy    846  AGAAGGTATCCAAGTTGGTGGGAGTCAGGAATCCAGTTCATGGAAGATGGCAG   905
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    950  AGAACGTCTCAAAGTTGGTTGGAGTCAGGAATTCAGTTTATGGATGAGGCCAG   1009

Qy    906  TATTTCTGCAGAATGCCAAGACCCGTTGCAAAAGATCGTGGAAGCATCAAATCTCAATA   965
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1010  TGTTTCTGCAGAATGCCAAGGCTAAAAAAAATCTCGGGAAGCATCAAAAGGCATTTC   1069

Qy    966  AGATGGAGGAAACTAGAACAGCAAGGTTATGAGATCATGAGCAACTCACTGTCAATCTCAATA   1025
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1070  AGATTGGAGAAAATAGGAACATGGCTATGAGAACATGAACCACTTCAGTGAGAGTTTG   1129

Qy   1026  GAGAGGAAAAAATTATCCGTGAAAATTGACTTTTTCTAGAGGAAGGAGAGAGAAAGAAGAGTG   1085
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1130  GAGAGAAGAAAGATAATATACGTGAAAATGACTTTTCAGAAGGAAGGATGAAAGAAGAG   1189

Qy   1086  CAGGACAAATAGATGAAGAAGAGAGAGAGGAGA-----------GGATGCAGTAGAAG   1130
           || |||||||||||||||||||||||||||           || |||||||||||
Db   1190  AAGAGGCGGAGGAGGAGAAAAAAGAGAGGAAGAAGTGGAACAGTAGAAG   1249

Qy   1131  TAGGAAGAGGCCAGAAAAATGTTCAAATAGCATCTTCAGGGAAAGAGCAGGAGTCTGGGAAAG   1190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1250  TGGAAGAGGTAGAAAATGTTCAAAACAGAAGAGTTTCCAGAGAAGAAAACCCAGAAAAAG   1309
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Qy    1191  CTGCAGAGCCCTCTCAGCTTCCCGCAGAGCTTCAGTCGTCGCCCCAGAGCCCACTACCTGCTT 1250
            ||||||||||||||||||||||| ||||||||||||||| |||||
Db    1310  CTTCAGAGCGTCTCTCAG------GTGGAGCTGCAGGCTGCCCCCTGGGGCACTTCCAGTTT 1363

Qy    1251  CCTCTCCAGGACCGTTTTCATCCATGCAGATGTCCTGGTGACACAG 1306
            ||| |||||||||||||||||||| ||||||
Db    1364  CCTCTCCAGGAGCCCACCTGCTGGGGGATGCCCCTGTGACACAG 1419
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RESULT 6
US-10-104-047-433
; Sequence 433, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: H1-A0105
; FILE REFERENCE: No. US20030236392A1e1 full length cDNA
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 433
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-433

Query Match   35.2%; Score 910.8; DB 17; Length 2634;
Best Local Similarity   84.2%; Pred. No. 1.3e-234;
Matches 1058; Conservative   0; Mismatches 177; Indels   21; Gaps   2;

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Qy      66  GGGACACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGA 125
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63  GGGACAGGGAGGAGAGAGCCCATCTCTCTGAATTACAAATCTTTTCTCCAGAGACAGCAGAG 122

Qy     126  CCATGGATAACTTGGAAAAAGCAAACTGATCTGTCCCATCTGCCTAGAGATGTTCACGAAGC 185
            ||||||||||||  ||  ||| |||||||| |||||||||| ||| |||||| |||||||||
Db     423  CCATGGATAACTTAGAGAAAGCAAACTCATCTGTCGTCCATCTGCTTAGAGATGTTCACGAAAC 482

Qy     186  CTGTGGTCATTCTCCCTTGCCAGCACAAACCTGTGCAGGAGAAAATGTGCACACATCTTCC 245
            || |||||||  ||||||||||||||||||||||||||||||| ||||||||||||||||
Db     483  CTGTGGTGATTCTCCCTTGTCAGCACAAACCTGTAGAAATGTGCCAGTGATATTTTTCC 542

Qy     246  AGGGCCTTCTAACCCGTACTTACCCACAAGAGGAGGCACCACCGTGGGCATCAGGGGCGCGCT 305
            |||||||| ||||||||| |||||||||| ||||||||  | | |||||| || |||  ||||
Db     543  AGGGCCTTCTAACCCGTATTTGCCCACACAGAGGAGGTACCACCATGGCATCAGGGGACTTGCCGAT 602

Qy     306  TCCGGCTGTCCCTCCTGCAGACACATGAGGTGGTGTTAGACACAGATGTCTATGGACTTGC 365
            |||||||||||||||||||| || | |||||||||||||| ||||||| | |||||||||
Db     603  TCCGGCTGCCCATCCTGTAGACATGAAGTGGTTTTGGATAGACATGGGGTATATGGGACTTC 662

Qy     366  AGAGGAGAACCTCTCGTGGGAAAAACATTATTGATTATCTACACAGCAGGAGAATCCACCCAGCCAG 425
            |||||||||||||||||||||| ||||||| || ||| ||||||||||||||||||  ||||||||
Db     663  AGAGGAACCTGCTGGTCTGGAAAATATCATTGACATCTACAAGCAGGAGTCCACCAGGCCAG 722

Qy     426  AAAAAAAAATTGGACACAGCCCCATGTGTGAAGAGACAGCATGAGAGAAGGAAACGCAATCAACTCAACTCTATT 485
            ||||||||||||||| ||||||||||||||| |||||| ||||||| ||  ||||||| | ||||
Db     723  AAAAGAAATCCGACACGCCCATGTGGAACATGAAGAGTCCACCAGGCCAG 782

Qy     486  GTCTGAACTGTGAAGTGCCCACCGTGTTCCTTCCTTGTGCAAGGTTTTTTGGCGGCCCCATAAGGACT 545
            |||||||||||||||||||||||||| ||| ||| ||| ||||||||  |||||||||||||||
Db     783  GTCTGAACTGGAAGTACCCACCGTTGTTGGTTGCCAGAAGGTCTCACACAAGGACT 842

Qy     546  GCCAGGTGGGCTCCCCGACTCATGTGTTCCAGACAGGAAGTCCAGCTCAGTGATGGTA 605
            ||||||||||||  |||||||||||||| ||| |||||||||| |||| |||||
Db     843  GCCAGGTGGCTCCCCTCACTCANTGTGTTCCAGACAGTGGAGGACA 902

Qy     606  TTGCTGTACTTGTGGGAAGCAACGATAGAGTTCCAGGGGTTGGATTCAGGCCAGGACA 665
            |||||||||||||||||||||||||| ||||| || |||| |||||||| ||||||||||
Db     903  TCGCCATCCTCGTGGGCAGCAACGATCGAGTCGATGCCAGCTGGAAGAGACA 962
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Qy   666 CCTGTAAAACTATTGAGGAGTGCTGCAGCGAGAAAGCAGGAAGCAGGAAGCAGGAGGACTTGCGTGTGAGAAATTG 725
           | ||| ||||||||||||||||||||||||||||||||||||||||
Db   963 CCTGCAAAACTATATCGAGGAATGTTGCAGCGAGAAAAGCAGAGAAATGACCCAAAGCCATCACTCGA 1022

RESULT 7
US-10-723-860-7135
; Sequence 7135, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;   Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7135
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7135

Query Match   35.2%; Score 910.8; DB 20; Length 2662;
Best Local Similarity   84.2%; Pred. No. 1.3e-234;
Matches 1058; Conservative   0; Mismatches 177; Indels   21; Gaps   2;

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Qy      66  GGGACACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTCCAAAGAGCAGCAGA 125
```

RESULT 8
US-09-764-864-34
; Sequence 34, Application US/09764864
; Patent No. US20020133753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-34

Query Match   34.7%; Score 899.8; DB 9; Length 1762;
Best Local Similarity   84.2%; Pred. No. 9.4e-232;
Matches 1058; Conservative 0; Mismatches 177; Indels 22; Gaps 3;

Qy   66 GGGACCGGCAAGGAAATGAGAGCACTTCTCTGAATTACAAGTCTTTCTTCTCCAAAGAGCAGCAGA 125
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   143 GGGACCGGCAAGGAAATGAGAGCACTTCTCTGAATTACAAGTCTTTCTTCTCCAAAGAGCAGCAGA 202

Qy   126 CCATGGATAACTTGGAAAAGCAACAACTGATTCGTGTTGCCAATCTCTGAATTACAAATCTTTT 185
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   203 CCATGGATAACTTAGAGAAGAGCAACTCATCTGTTGCCCATCTGTTTGGGGATTATATGGACTT 262

Qy   186 CTGTGTGGT-CATTCTCCCTTGCCAGACGACAACCTGTGCCACTGTCCTGGTGACATCTTTC 244
         ||||||||| |||||||||||||||||| ||||| |||||||||||||||| | |||||||
Db   263 CTGTGGTAGATTCTCCCTTGTCAGACACAACCTGTGTAGGAGATGTGCCAGTGATATTTTTC 322

Qy   245 CAGAGGGAACCTGCGTGGTGGAAAACATTATTGATATCTACAAGCAGCAGGAATCCACCAGGCCA 304
         ||||||||||||||||||||||||| || | |||||| ||||||||||||||||| |||||||||
Db   323 CAGGCCTCTAACCCGTATTTTGCCCACAAGAGGAGTACCACCAAGCCATCAACATCTCACCAGCA 382

Qy   305 CAGGCCTCTAACCCGTACTTACCCACAAGAGGAGTACCACCAAGCCATCAACATCTAT 364
         ||||||||||||||||| |||||||||||||||||||| ||||||||| ||||||||
Db   383 TTCCGCTGCCCATCCCATCTGTGACACATGAAAGTGGGGTATATGGGACT 442

Qy   365 CAGAGGCGAACCTGCGTGGTGGAAAATGTTGACATCTTC 424
Db   443 ...

```
Qy    665  ACCTGTAAAACTATTGAGGAGTGCTGCAGAAAGCAGAAACCTGTGTTGAGAAATTT  724
           |||||  ||| ||||||||| ||||||||||||||  ||||||  |||||||||||||
Db    743  ACCTGCAAAAACTATCGAGGAATGTTGCAGAAAACACGAAAGAGCTTTGTGAGAAGTTT  802

Qy    725  GATCACCTATACGGCATCCTCGGAGGAGGAGGACTGAAAATGACCCAAGCCATCACTCGA  784
           ||| ||| ||||||  ||||                                           
Db    803  GATTACCTGTATGGCATTTTGGAGGAGGAGGAAGAATGAAAATGACCCAAGTCATTACCCGA  862

Qy    785  ACACAGGAGGAGAAACTGGAACATGTTCCGAACTCTTATCTCAGGAAGTATTTCGGATCACCTG  844
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    863  ACCCAAGAGGAGAAACTGGAACATGTTCCGGTCTCTGATCAAAAAGTATTCTGATCATTTG  922

Qy    845  GAGAAGCTATCCAAGTTGGTGGAGTCAGGAATCCAGTTCATGGAGTCAGCCCGAAATGGCA  904
           |||||| ||  ||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    923  GAGAAGCTCTCAAAGTTGGTTGAGTCAGGAATTCAGTTTATGGATGAGTCCCAGAAAATGGCA  982

Qy    905  GTATTTCTGCAGAATCCCAGACACCCTGTTGCAAAAAGATCGTGGAACATCAAAAGCGTTT  964
           ||||||||||||||||| |||| ||| ||||||||||||||||||||| |||||| ||||||
Db    983  GTGTTTCTGCAGAATGCCAAAAACCCTCTAAAAAAAAAATCTCAGAAGCATCAAAGGCATTT  1042

Qy    965  CAGATGCGGAGAAACTAGAACAAAGGTTATTGAGAATCATGAGCAACTTCACTGTCAATCTCAAT  1024
           ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |||| ||
Db    1043 CAGATGCGGAGAAATAGAACATGGCTATGAGAACATGAACCACTTCACAGTCAACTTCAAT  1102

Qy    1025 AGAGAAGAGAAAAATTATCCGTGAAAATTGACTTTTCTTAGAGAAGAGGAGGAAGAAGAGAT  1084
           ||||||||||||||||||||||||||  ||||||||||||||||||| |||||||||||||
Db    1103 AGAGAAGAAAAAGATAATAACGTTGAAAAATTGACTTTTACGAGAAGATGAAGAAGAAGAA  1162

Qy    1085 GCAGGAGAAATAGATGAAGAAGGAGGAGAGGGAGA---------------GGATGCAGTAGAA  1129
           ||||||||||||| ||||||||||||||||||||||                |||||||||||
Db    1163 GAAGAAGAGGCGGAGAAGGAGGAAGGAGTGGGAGGAGGAGGAAGGA----GGATGCAGTAGAA  1222

Qy    1130 GTAGAAGAGGCCAGAAAATGTTCAAAATAGCATCTTCAGGGAGAAGAGAGTCTTGGAGAA  1189
           |||||||| | ||||||| | | ||||||||| | |||||||||||||||||  |||||||
Db    1223 GTGGGAAGAGGTAGAAAAATGTTCAAAACAGAGTTTTCAGGAGAAGATGAAAAACCCAGAAAAA  1282

Qy    1190 GCTGCGAGAGCCCTCTCAGCTTCCCGCAGAGAGCTTCAGGTCCTGCGCCCCAGAGCCACTACCTGCT  1249
           ||  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    1283 GCTTCAGAGCTCTCTCAG-----GTGGAGCTGCGCAGGCTGCCCCTGGGGGCACTTCCAGTT  1336

Qy    1250 TCCTCTCCAGAACCGTTTTCATCCANGCCACCTGCTCGCGAGATGTCTTCGGGTGACACAG  1306
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    1337 TCCTCTCCAGAGACCACCTGCTTCCACCCTTGCTCGCGGGATGCCCCTGTGACACACAG  1393
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RESULT 9
US-10-204-921-12
Sequence 12, Application US/10204921
Publication No. US20050095587A1

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Query Match       18.7%;  Score 485.6;  DB 21;  Length 2110;
Best Local Similarity   67.7%;  Pred. No. 8.1e-120;
Matches  696;  Conservative   0;  Mismatches  329;  Indels   3;  Gaps   1;
```

```
Qy    112  CAAAGAGCAGAGACCATGGANTAACTTGGAAAAGCAACTGATCTGTCCAATCTGCCTAGA  171
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||
Db    148  CCAGGATGGGAGAATCCCATGGAGAACTTGGAGAAGCAGCTGATCTGCCCTATCTGCCTGGA  207

Qy    172  GATGTTCACGNAGCCTGTGGTCATTCTCCCTTGCCAGCCAGCACCTGTGTCAGGAAATGTGC  231
           ||||||||  | |||||||| |||||||||||||||||||||||| ||||||| ||||||
Db    208  GATGTTTACCAAGCCAGTGGTCATCCTTTGCCCTTGCCAGCCAGCACAACCTGTGCCGGAAGTGTGC  267

Qy    232  CAGTGACATCTTCCAGGCCTCTAACCCGTACTTACCCACAAGAGGAGGACCACACCCTGGC  291
           |||||||||||||||||||||||||||  || |||||  || ||||||| || ||||||||
Db    268  CAATGATATTTTCCAGGCCTCTTAAACCCGTATTTGCCCACAAGAGGAGGTACCACCACCTGGC  327

Qy    292  ATCAGGGGACGGGCCGCTTCCGGCTGTCCCTCCCCTGCAGACACATGAGGTGGTGGTTAGGACAGAGACATGG  351
           |||||||||| |||||||| || ||||  || | || || ||| || || |||||||| ||||||||||||
Db    328  ATCAGGGGCGGGCCGGATTCCGCTCGCCACCCTGTAGACATGGAAGTGGTTTTGGATAGACACATGG  387

Qy    352  GGTCTATGGACTGCAGGAGAACCTGCTCGTGGGAAAAACATTATTGTAATCTACAGCAGGA  411
           |||||| || || |||||||||| |||| |||||||||||||||| |||| |||||||||||
Db    388  GGTATATGGACTTCAGAGGAACCTGCTTGGTGGAGAAACATCATCGACATCTACAAAACAGGA  447

Qy    412  ATCCACCA---GGCCAGAAAAAAAATTGGACCAGCCCATGTGTGAAGAGCATGAAGAGGA  468
           |  | ||||   |||||||||||||  || ||||| || || ||||||||||| ||||||
Db    448  GTGCTCCAGTCGGCCGGCTGCAGAAGGGCAGTCACCCCATGTCCAAGAGCACGAAGGATGA  507

Qy    469  ACGCATCAACATCTATTGTCNGAACTGTGAAGTGCCCACCTGTTCCTTGTCGGCAAGGTTTT  528
           |||||||||||||||||| | ||||| ||| || |||||| || |||||||| ||||| |||
Db    508  GAAAATCAACATCTACTGTGTCTCACGTGTGGAGGTGCCACCTCCACCGTGCTCCAAGGTTGT  567

Qy    529  TGGCGCCCATAAGGACTGCCAGGTGGCTCCCGTCATGTTGTTCCAGAGCAGGAGGAGTC  588
           |||||| ||||||||||| |||||| ||| |  || || || |||||| || ||||||||
Db    568  TGGGATCCACAAGGCCTGCGAGGTGCGCCCCATTGCAGAGAGTGTCTTCCAGGGACAAAAGAC  627

Qy    589  AGAGCTCAGTGATGGGTATTGCTGTACTTGTGGGAGAGCCAACCAACCATAGAGTCAGGGGTGAT  648
           | |  |||||| ||| ||| ||||| || |||||||||||| |||||||||  ||||| |||
Db    628  TGAACTGAATAACTGTATCTCCATGCTGGTGGTGGCGGGGAATGACCGTGTGTGCAGAACCAT  687

Qy    649  CAGCCAGCCTGGAGGACACCCTGTAAAACTATTGATGAGGAGTGCTGCAGAAAGCAGAAAACAGGA  708
           ||||||||| |||||||||  || ||| ||||||||||||||||||| |||||||| |||| ||||
Db    688  CAGCCAGCCTGGAGGCCACCCTGTAAAACTATTGATGAGGAGTGCTGCAGAAAGCAGAAAACAGGA  708
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```
RSULT 10
US-09-890-688-57
; Sequence 57, Application US/09890688
; Publication No. US20030144475A1
; GENERAL INFORMATION:
; APPLICANT: Seishi KATO
; APPLICANT: Chikashi EGUCHI
; APPLICANT: Mihoro SAEKI
; TITLE OF INVENTION: Human Proteins and cDNAs thereof
; FILE REFERENCE: 2001-1102A/WMC/00653
; CURRENT APPLICATION NUMBER: US/09/890,688
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: JP 11-346863
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 11-34684
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: JP 2000-31062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34091
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: JP 2000-34090
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: JP 2000-35829
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-35899
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 2000-71161
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: JP 2000-160851
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1913
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (303)..(1379)
US-09-890-688-57

Query Match             17.8%;  Score 461;  DB 10;  Length 1913;
Best Local Similarity   65.0%;  Pred. No. 3.4e-113;
Matches  699;  Conservative    0;  Mismatches  370;  Indels    6;  Gaps    1;
```

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Qy    62 GACAGGGACGGCAAGGAAATGAGCACTTCTCTGAATTACAAGTCTTTCTGAATGGCC 121
Db   285 GGCACGACCACCACGGAGGGGATGAACTTCACAGTGGGTTTCAAGCCCGTGCTTAGGGGATGCA 344

Qy   122 CAGACCATGATAACTTGGAAAAGCAACAACTGATCTCTGCCTCATCTGCCTAGAGAT GTTCACG 181
Db   345 CACAGCATGGACAACCCTGGAGAAGCAGCCTCAATCCTGGGAGATGGTTTCCC 404

Qy   182 AAGCCTGGTGGTCATTCTCCCTTGCCAGCCACCACAACCTGTGTCGCAGGAAATGTTGCCAGTC 241
Db   405 AAACCAGTGTGATCTGATCCTGCCCTGCCCACAACCTGTGCCGCCAAACGACGTC 464

Qy   242 TTCCAGGCCTCTAACCCGTACTTACCCACAAGAGGAGGAGGCACACCGTGGCATCAGGGGC 301
Db   465 TTCCAAGCCTCGAAATCCTCTATGGGCAGTCCCCGGAGGTCCCAAGGC 524

Qy   302 CGCTTCCGCTGTCCCTCCTCGCAGACATGAGGTGGTTGTTAGAGTGGGGTCATGGA 361
Db   525 CGTTTCCGCTGCCCATCGTGCAGAGAAGCCATGAGGTGTCCCTGGACAGAGAGCTGCGGC 584

Qy   362 CTGCAGAGGAACCTGCGTCGTGGAAAACATTATTGATATCTACAAGCAGGAATCACCAGG 421
Db   585 CTGCAGCGAAACCTGCTAGTGTGGAGAACATTATCAGACATTTACAGCAGGAGTCATCCAGG 644

Qy   422 CC------AGAAAAAATTGGACCAGCCCATGTGTGAAAGCATGAAGAGGAACCGATC 475
Db   645 CCGCTTGCACTCCAAGGCTGAGCAGCCACCTCAATGTGCGGAGGGCCATGAAGAGAGAAGAGATC 704

Qy   476 AACACTATTGTTCTGAAACTATGGGCCCACCCTGTTCCTTGTTGCAAGGTTTTTTGCGCC 535
Db   705 AATATTTTACTGCCTGAGCTGTGAGCTGCCCACCTGCAAGGTCTTCGGTGCC 764

Qy   536 CATAAGGACTTGCCAGGTGAGGCTCCCCTGACTCATCATGTGTTCCAGAGGCCAGGGAGCTC 595
Db   765 CACAAGGACTGTGAGGTGGCCCCACTGCCCCACCATTACAAACGCACAGAGAGTGAGCTC 824

Qy   596 AGTGATGGTATTGCTGTTACTTGTGGCAAGCAACGATAGAGTGCCAGGGTGTGATCAGCAG 655
Db   825 AGCGGATGGCATCGCGATGCTCGGTGGCCAGGCAAATGACCGCGTGGCAAGGCAGTGAATCACACAG 884

Qy   656 CTTGGAGGACACACCTGTAAAACTATTCAGGGATTCGCAGAAAGCAGGACCTGTGT 715
Db   885 ATGGAGGAGCGTGTGCCAGACTATCGAGGACTATAGCCGACGGAGAGTAAAC 944

Qy   716 GAGAGAAATTTGATCACCTATACGGCATCCTGGAGGAGGAGGAGGAAATGACCAAGCC 775
Db   945 CAGAGGTTTGAGAGCCTTGTCGCGCAGTCGCTGGAGGAGGTTGAGCTTGCTGCAGGCG 1004

Qy   776 ATCACTCGACACAGGAGGAGAACTGGACACATGTCCGGACACTCTTATCAGAAGTATTCC 835
Db  1005 CTGGCCCCGGAGCAAGAGGAGGAAGCTGCACGCGTGTCCATCAGTATGGC 1064

Qy   836 GATCACCTGAGAACGTATCCAAGTTGGTGGTGGAAGTCAGGATGAGCC 895
Db  1065 GACCACCTGAGGCCTCCCTCCTAAGCTGGTGCCATCGAGTCAGGAAGAGCCA 1124

Qy   896 GAAATGGCACAGTATTTCTGCAGAATGGCCAAGACCCTGTTGCAAAAGAATCGTTGGAAGCATCA 955
Db  1125 CAAATGGCGCTGTGTATCTCCAGCAGCGCTGGATCAATAAGGTCGGGGCCTATGTC 1184

Qy   956 AAGGCGTTTCAGATGGAGAACAAGCAAGGTTATGAGATCATGAGCAACTTCACTGTC 1015
Db  1185 AAGGTGGAGCTGGCAGGGGCCGGGGCCAGGGCTATGAGAGCAATTCACCGTA 1244

Qy  1016 AATCTCAATAGAGAGAGAGAGAGAGAGAAAATATCCGTGAAATTGACTTTCTGAGAAGAGGAGAAGAG 1075
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Db   688 CACTCAGCTGGGAGGAGATTCCCGTCGAGTGACCAAGAGAGAACGCAGTCACCAGTGAAAGGAAGA 747
Qy   709 CCTGTGTGAGAAAATTTGATCACCTATACGGCCATCCTGGACGGAGGAGGAGGAAGATGAAAGATGAC 768
Db   748 GCTGAGCCAGAAGTTTGACAGGTTGTATGCCCATCCTGGATGAGAGAGAAAAGTGAGTTGCT 807
Qy   769 CCAAGCCATCACTCGAACACAGGAGGAGGAGAAACTGAACACATGTCCGAACTCTTATCAGGAA 828
Db   808 GCAGGGGATCACGCAGGAGGACAGGAGGAGAAAAAGCTTAGCTGTTCATCGAGGCCATCCTGGA 867
Qy   829 GTATTCCGATCACCTTGGAGAACGTATCCAAGTTGGTGGTGGAGTCAGGAATCCAGTTCATGGA 888
Db   868 GTACCAGGGATCCAGCTGGACAAGTCCACAAAGCTGGTTGGGAAACTGCCATCCAGTCCCATCCAGCA 927
Qy   889 TGAGCCCGAAAATGGCAGTAGTATTTCTGCAGAATGCCAAGAGACCCTGTTGCAAAAGGATCGTGGA 948
Db   928 CGAGCCTGGGGAGCGAGCCACCTTCCTCTTGACTCGCCAAGCACTCATCATCAAAAAGCAGACTTGGA 987
Qy   949 AGCATCAAAAGGGCGTTTCAGATGGAGAACAAGGTTATGAGATCATGAGCAACTT 1008
Db   988 AGCTTCCAAGGGCTGCCCAGCTGGGAAGACGAGAGGCTTTGAGAACAATGGACACTTCTT 1047
Qy  1009 CACTGTCAATCTCAATAGAGAGAAAAAATTATCCGTGAAATTGACTTTCTAGAGAAGA 1068
Db  1048 TACTTTGGATTTAGAGCACATAGCAGAGACGCCCCTGAGAGCCCATTGACTTTGGGACAGATGA 1107
Qy  1069 GGAGAGGAGGAAGAGAGATGCAGGAGGAAATAGATGAGAGAGAGAAGAGGAGGAGAAGTGCAGTGAGA 1128
Db  1108 GGACAGGAGGAAGAATTCATTGAAGAGAAGATCAGGAGAGAGTCCACAGAGAAGGGAA 1167
Qy  1129 AGTAGAAG 1136
Db  1168 GGAGAGAAG 1175
```

RESULT 11
US-10-061-043A-20
; Sequence 20, Application US/10061043A
; Publication No. US20030129686A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753B
; CURRENT APPLICATION NUMBER: US/10/061,043A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 20
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: rat
US-10-061-043A-20

Query Match   17.5%; Score 452; DB 15; Length 1053;
Best Local Similarity   66.1%; Pred. No. 6.4e-111;
Matches 669; Conservative   0; Mismatches 340; Indels   3; Gaps   1;

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Qy    126 CCATGGATAACTTGGAAAAGCAACACTGATCTGTCGTCCATCTGCCTAGAGATGTTCACGAAGC 185
              ||||| || |||||| |||||| ||   ||||| ||||||||||| |||||||| || |||||
Db     38 CTATGGAGAAACCTGGAGAAGCAGCTCATCTGCCCATCTGCCTTGAGATGTTTACCAAGC 97

Qy    186 CTGTGGTCATTCTCCCTTGCCAGCACAACCTGTGCACCAGGAAATGTGCAGTGAACATCTTCC 245
           |||||||||| || |||| ||||||||||||| || |   ||||| ||||| |  |||||||||
Db     98 CTGTGGTCATCCTGCCCTGCCAGCACAACCTCTGCCCGGAAGTGTGCGACATCTTCC 157

Qy    246 AGGGCCTCTAACCCGTACTTACCCACAAGAGAGGAGGCCACGT 305
           ||| | |  ||||| ||||| |  ||| |||| |||||  |
Db    158 AGGCTGCCAATCCCTACTTGGACCAACCGCGTGGGTCCCA 217

Qy    306 TCCGCTGTCCCTCCTCCGCAGACAATGAGGTGGTTGTTAGACAGACTCTTATGGACTGC 365
           ||||| || |||| |||||  |||||||  ||| ||| |||| |  |  |||| |||||
Db    218 TCCGCTGCCCCTTCGTTGCCCGGCCCATGAAGTTGAICATGAGG 277

Qy    366 AGAGGAACCTGCTTCGTGGGAAAACACATTATTGATATCTACAACAGCAGGAATCCACCA---GGC 422
           |||||||  |||||||||    ||||| ||| || |  | ||| || ||||| |  ||||    |||
Db    278 AGAGGAAACCTGCTGGTGGTGGAACATCATCGACAAGGAAGAGGAATGCTTCCAGTTGGC 337

Qy    423 CAGAAAAAAATTGGACCAGCGCCATGTGTGAAGAGCATGAGAGGAACGCATCAACATCT 482
           |||||  |||||| ||| |||||| | |||||||| |||| ||||| ||||| || |||
Db    338 CCCTGCAGAAAGGCACCCGATGTGTGCAGGAGACGAAGAAAATCAACATCT 397

Qy    483 ATTGTCTGAACTGTGAAGTGCCCACCTGTTCCTTGTCTGCAGGTTTTGGCGCCCATAAGG 542
           ||||| ||||||||||| ||||||| |||||||| |  ||| || || |  ||||| |||
Db    398 ACTGTCTCACGTGCGAGGTGCTTCCTACTTGCTCCGGGCTCAAGAGAC 457

Qy    543 ACTGCCAGGTGGCTCCCCCTGACTCATGTGTTCCAGGACGAGAGTCAGAGCTCAGTGATG 602
           ||||||||| ||| ||  ||| || |||||||| || ||| || |||| || |||| |||
Db    458 CCTGTGAAGTTGCCCCTTACAAAGCATCTCCAAGGACAGAAGACTGAACTGAGCAATT 517

Qy    603 GTATTGCTGTACTTGTGGGGAAGCAACGATAGAGTCCAGGTGTGTCAGCCAGCTGGAGG 662
           ||||| ||| ||| ||||| |||||| |  | | ||||| |||| |||  ||||||||||
Db    518 GCATCTCCATCGTCTGGTGCGTGGCAGGGAACGACACCGAGTTCAGACTATCACTCGCAGCTGGAGG 577
```

RESULT 12
US-10-060-634C-20
; Sequence 20, Application US/10060634C
; Publication No. US20030219739A1
; GENERAL INFORMATION:
; APPLICANT: Glass, David
; APPLICANT: Bodine, Sue
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND POLYPEPTIDE MOLECULES
; FILE REFERENCE: REG 753A
; CURRENT APPLICATION NUMBER: US/10/060,634C
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/338,742
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/311,697
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/264,926
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 20
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: rat
US-10-060-634C-20

Query Match   17.5%; Score 452; DB 17; Length 1053;
Best Local Similarity   66.1%; Pred. No. 6.4e-111;
Matches 669; Conservative   0; Mismatches 340; Indels   3; Gaps   1;

```
Qy    663 ACACCTTGTAAAACTATTGAGGAGTGCTGCAGAAAAGCAGAAAACGACCTGTGTGAGAAAT 722
           |||||| | |  ||| ||||| ||||| |||||||| |||||| ||   ||||| |||||||
Db    578 ACTCCTTGCCGAGTGCACCTGGAGAAAAACAGCCACCAGGTGAAGGAGAACCCATCACTC 637

Qy    723 TTGATCACTTACCTGGCATCCTGGAGGAGAAACAGCCATCCAGTTGGTGGAGTCAGGAA 782
           |||| |||| ||| || || |||||| |||| ||||||| |||| |||||| |||||
Db    638 TTGACGCCCTCTACGGCCATCCTGGACGGAGAAGAGAAGAGAGTGAGCTGCTCC 697

Qy    783 GAACACAGGAGGAGAAACTGGAACATGTCCGAACTCTTATCTGGAAGTATTCCGGATCACC 842
           ||  ||||||||| ||  ||||| ||||| |||  ||| || |||| || |||| |||||||
Db    698 AGGAGCAGGAGGAAGCTGGACTTCATCGAGCAAGCTGATCCTCCAGTACCCGAGAGCAGT 757

Qy    843 TGGAGAACGTATCCAAGTTGGTGTGAGTCAGGAATCCAGTTCATGGATGAGCCCGAAATGG 902
           |||| ||||||| ||| ||||| |||||||| || |||||| ||||| ||| || |||||||
Db    758 TGGAAAAGTCGACCAAGCTGTGGGAAAACAGCCATCCAGTCCCCGCCTTGGAAATCTGGAGGG 817

Qy    903 CAGTATTTCTGCAGAATGCCAAGACCCTGTTGCAAAAGATAGTGGAAGCATCAAAAGCCGT 962
           ||| | ||||| |||| || ||||||| || | ||||||| ||||| |||| || ||||||
Db    818 CCACCTTCCTCTTGAGTGCCGAAGCCCGCTCATCAAAGAGCAATTGTTAGAAGCTTCCAAGGGCT 877

Qy    963 TTCAGATGGAGAAACTAGAACAGAAGGTTATGAGATCATGAGCAAACTTCACTGTTCCATCTCA 1022
           || || || ||||| || |  || || || |||| || ||||||| || | |||| |||||||||
Db    878 GCCAGCTGGGGAGAACAGAGGAAGGCTTTGAGAACATGGACTACTTTACTCTGAAATTTAG 937

Qy   1023 ATAGGAGAAGAAAATTATCCCGTGAAATTGACTTTTCTAGAGAAGGAGGAGGAGGAGAAG 1082
           || || |||| || ||||| ||||| || ||| ||| |||| || ||| |  |||| | ||
Db    938 AACACAATAGCAGGAGGCCTTGAGGGCCATCGACTTTGGGACAGATGAGGAGGAGGAGGTTA 997

Qy   1083 ATGCAGGAGAAATAGATGAAGAGGAGGAGGAGGAAGATGCAGTAGAGAAGTAGA 1134
           |||  ||| ||||   ||| |||||| || || |||| ||||||| |||||
Db    998 CTGAAGAGCAGGAGGAGGAGGAATCAAGAAGAGAGAGAGAGGAGGCGGTTGTCCACAGAGGAGGGACA 1049
```

RESULT 11 (continued)

```
Qy   1245 CCATGGATAACTTGGAAAAGCAACACTGATCTGTCCATCTGCCTTCCGGG
               |||||     |  |  | |  | | | |  ||   | |  | |
Db   1305 GAGGAGAAGGAGGTGCCCCAGCGAGGAGGAGGAAG 1359
```

```
Qy   1076 GAAGAAGATGCAGGAGGAGAAATAGATGAAGAAGGAGGAGGAGTAGGAG 1130
           |||||||| |  |   |  | |  || |    | | |  |  |  |||||
Db   1304
```